

Mohamed, A.
091863600

09/863600

FILE 'REGISTRY' ENTERED AT 12:25:15 ON 06 NOV 2003
L1 4 S GGTASCHFGPLTWVCKPQGG/SQSP

L1 ANSWER 1 OF 4 REGISTRY COPYRIGHT 2003 ACS on STN
RN 243125-13-5 REGISTRY
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cyclic (6-15)-disulfide (9CI) (CA INDEX NAME)
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RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 131:209282

L1 ANSWER 2 OF 4 REGISTRY COPYRIGHT 2003 ACS on STN
RN 209594-31-0 REGISTRY
CN Glycinamide, glycylglycyl-L-threonyl-L-alanyl-L-seryl-L-cysteiny-L-
histidyl-L-phenylalanylglycyl-L-prolyl-L-leucyl-L-threonyl-L-
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SEQ 1 GGTASCHFGP LTWVCKPQGG
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HITS AT: 1-20

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 129:90879

L1 ANSWER 3 OF 4 REGISTRY COPYRIGHT 2003 ACS on STN
RN 203397-46-0 REGISTRY
CN Glycine, glycylglycyl-L-threonyl-L-alanyl-L-seryl-L-cysteiny-L-
histidyl-L-phenylalanylglycyl-L-prolyl-L-leucyl-L-threonyl-L-
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cyclic (6-15)-disulfide (9CI) (CA INDEX NAME)
SQL 20

SEQ 1 GGTASCHFGP LTWVCKPQGG
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HITS AT: 1-20

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 128:176424

L1 ANSWER 4 OF 4 REGISTRY COPYRIGHT 2003 ACS on STN
RN 186526-47-6 REGISTRY
CN Glycine, glycylglycyl-L-threonyl-L-alanyl-L-seryl-L-cysteiny-L-
histidyl-L-phenylalanylglycyl-L-prolyl-L-leucyl-L-threonyl-L-
tryptophyl-L-valyl-L-cysteiny-L-lysyl-L-prolyl-L-glutaminyglycyl-
(9CI) (CA INDEX NAME)
OTHER NAMES:

09/863600

CN 13: PN: WO0191780 SEQID: 19 claimed protein
SQL 20

SEQ 1 GGTASCHFGP LTWVCKPQGG
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HITS AT: 1-20

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 136:32169

REFERENCE 2: 130:61259

REFERENCE 3: 130:493

REFERENCE 4: 126:152802

FILE 'HCAPLUS' ENTERED AT 12:26:08 ON 06 NOV 2003
L2 7 S L1

L2 ANSWER 1 OF 7 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 2001:885800 HCAPLUS

DOCUMENT NUMBER: 136:32169

TITLE: Neuroprotective peptides that are peptide
mimetics of erythropoietin

INVENTOR(S): Smith-Swintosky, Virginia; Renzi, Michael;
Plata-Salaman, Carlos; Jolliffe, Linda; Farrell,
Francis; Johnson, Dana L.

PATENT ASSIGNEE(S): Ortho-McNeil Pharmaceutical, Inc., USA

SOURCE: PCT Int. Appl., 75 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
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WO 2001091780	A1	20011206	WO 2001-US16654	20010523
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG			
EP 1296702	A1	20030402	EP 2001-941562	20010523
R:	AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR			
US 2003130197	A1	20030710	US 2001-863600	20010523
PRIORITY APPLN. INFO.:			US 2000-207654P P	20000526
			WO 2001-US16654 W	20010523
OTHER SOURCE(S):	MARPAT 136:32169			
AB	Methods of treating diseases of the nervous system by administration			

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of compns. having the neurol. therapeutic activity of human erythropoietin are disclosed. These compns. include therapeutic agents such as peptides, peptide dimers, polypeptides, and proteins that have the full range of biol. activity of human erythropoietin or only certain biol. activities of erythropoietin. Improved therapeutic regimens where the erythropoietin is administered at concns. below those required to stimulate hematopoiesis are also provided.

IT 186526-47-6

RL: PAC (Pharmacological activity); BIOL (Biological study)
(neuroprotective peptides that are peptide mimetics of erythropoietin)

REFERENCE COUNT: 1 THERE ARE 1 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 2 OF 7 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1999:396628 HCAPLUS

DOCUMENT NUMBER: 131:209282

TITLE: A peptide mimetic of erythropoietin: critical residues and description of a minimal functional epitope

AUTHOR(S): Johnson, Dana L.; Farrell, Francis X.; McMahon, Frank J.; Tullai, Jennifer; Barbone, Francis P.; Middleton, Steven A.; Hoey, Kenway; Livnah, Oded; Wrighton, Nicholas C.; Dower, William J.; Mulcahy, Linda S.; Stura, Enrico A.; Wilson, Ian A.; Jolliffe, Linda K.

CORPORATE SOURCE: Drug Discovery Research, The R. W. Johnson Pharmaceutical Research Inst., Raritan, NJ, USA

SOURCE: Peptides: Frontiers of Peptide Science, Proceedings of the American Peptide Symposium, 15th, Nashville, June 14-19, 1997 (1999), Meeting Date 1997, 501-503. Editor(s): Tam, James P.; Kaumaya, Pravin T. P. Kluwer: Dordrecht, Neth.
CODEN: 67UCAR

DOCUMENT TYPE: Conference

LANGUAGE: English

AB Ala substitution in the conserved positions of EMP1 (GGTYSCHFGPLTWVCKPQGG), a peptide mimetic of erythropoietin, was done to determine the effect on both binding and mimetic activity in vitro. Most of the Ala substitutions decreased the relative binding affinity. Trp13 substitution had the most significant effect, resulting in almost undetectable binding and a complete loss of mimetic activity. Ala substitution of Tyr4, Gly9 or Thr12 each resulted in significant relative binding losses and a concomitant loss of mimetic action. Unexpectedly, Ala substitution of Pro10 had no effect on relative binding or mimetic activity suggesting that an acceptable β -turn structure can still be achieved. Substitution of Pro17 resulted in a 100-fold loss of mimetic activity. The relative binding of this peptide was also significantly altered and was limited by decreased peptide solubility. The two aromatic residues at positions Tyr4 and Trp13 appear to play important roles in both EPO receptor binding ability and EPO mimetic properties of EMP1. To investigate this further, Tyr4 or Trp13 was replaced with Phe. Restoration of aromaticity at position 4 resulted in the recovery of some binding activity (12-fold less than

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EMPl) and mimetic activity. Restoration of aromaticity at Trp13 resulted in recovery of activity to a level similar to EMPl. The data indicate that aromatic residues at these positions are important for EMPl agonist activity. The authors next sought to determine the minimal active structure within the EMPl sequence by truncating residues of the peptide outside the disulfide bond. YSCHFGPLTWVCK represents the minimal active structure identified.

IT **243125-13-5**

RL: BAC (Biological activity or effector, except adverse); BPR (Biological process); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); PROC (Process)
(peptide mimetic of erythropoietin, its critical residues and description of a minimal functional epitope)

REFERENCE COUNT: 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 3 OF 7 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1998:730721 HCAPLUS

DOCUMENT NUMBER: 130:61259

TITLE: An antagonist peptide-EPO receptor complex suggests that receptor dimerization is not sufficient for activation

AUTHOR(S): Livnah, Oded; Johnson, Dana L.; Stura, Enrico A.; Farrell, Francis X.; Barbone, Francis P.; You, Yun; Liu, Kathleen D.; Goldsmith, Mark A.; He, Wen; Krause, Christopher D.; Pestka, Sidney; Jolliffe, Linda K.; Wilson, Ian A.

CORPORATE SOURCE: Department of Molecular Biology and the Skaggs Institute for Chemical Biology, The Scripps Research Institute, La Jolla, CA, 92037, USA

SOURCE: Nature Structural Biology (1998), 5(11), 993-1004

CODEN: NSBIEW; ISSN: 1072-8368

PUBLISHER: Nature America

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Dimerization of the erythropoietin (EPO) receptor (EPOR), in the presence of either natural (EPO) or synthetic (EPO-mimetic peptides, EMPs) ligands is the principal extracellular event that leads to receptor activation. The crystal structure of the extracellular domain of EPOR bound to an inactive (antagonist) peptide at 2.7 Å resolution has unexpectedly revealed that dimerization still occurs, but the orientation between receptor mols. is altered relative to active (agonist) peptide complexes. Comparison of the biol. properties of agonist and antagonist EMPs with EPO suggests that the extracellular domain orientation is tightly coupled to the cytoplasmic signaling events and, hence, provides valuable new insights into the design of synthetic ligands for EPOR and other cytokine receptors.

IT **186526-47-6**

RL: BAC (Biological activity or effector, except adverse); BPR (Biological process); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); PROC (Process)
(EPO-mimetic peptides; antagonist peptide-EPO receptor complex suggests that receptor dimerization is not sufficient for activation)

REFERENCE COUNT: 45 THERE ARE 45 CITED REFERENCES AVAILABLE

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FOR THIS RECORD. ALL CITATIONS AVAILABLE
IN THE RE FORMAT

L2 ANSWER 4 OF 7 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1998:719126 HCAPLUS

DOCUMENT NUMBER: 130:493

TITLE: Methods of administering peptides that bind to
the erythropoietin receptor, and method for
therapeutic use

INVENTOR(S): Wrighton, Nicholas C.; Dower, William J.; Chang,
Ray S.; Kashyap, Arun K.

PATENT ASSIGNEE(S): Affymax Technologies N.V., UK

SOURCE: U.S., 103 pp., Cont.-in-part of U.S. Ser. No.
155,940, abandoned.

CODEN: USXXAM

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 3

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 5830851	A	19981103	US 1995-484631	19950607
CA 2223833	AA	19961219	CA 1996-2223833	19960607
WO 9640749	A1	19961219	WO 1996-US9810	19960607
W:	AL, AM, AT, AU, AZ, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG			
RW:	KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA			
AU 9661667	A1	19961230	AU 1996-61667	19960607
AU 712713	B2	19991111		
CN 1192748	A	19980909	CN 1996-196094	19960607
EP 886648	A1	19981230	EP 1996-919296	19960607
R:	AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI			
JP 11507367	T2	19990629	JP 1996-502023	19960607
BR 9609006	A	19991214	BR 1996-9006	19960607
PL 185040	B1	20030228	PL 1996-323858	19960607
NO 9705729	A	19980205	NO 1997-5729	19971205
PRIORITY APPLN. INFO.:			US 1993-155940	B2 19931119
			US 1995-484631	A 19950607
			US 1995-484635	A 19950607
			WO 1996-US9810	W 19960607

OTHER SOURCE(S): MARPAT 130:493

AB Peptides of 10 to 40 or more amino acid residues in length and having the sequence X3X4 X5GPX6TWX7X8 (X3 = C; X4 = R, H, L, W; X5 = M, F, I; X6 = any of 20 genetically coded L-amino acids; X7 = D, E, I, L, V; X8 = C), which bind and activate the erythropoietin receptor (EPO-R) or otherwise act as an EPO agonist, are provided, as are methods for their use in treating a patient with a deficiency of erythropoietin or a low or defective red blood cell population.

IT 186526-47-6

RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(peptides binding to erythropoietin receptor, and therapeutic

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use)
REFERENCE COUNT: 27 THERE ARE 27 CITED REFERENCES AVAILABLE
FOR THIS RECORD. ALL CITATIONS AVAILABLE
IN THE RE FORMAT

L2 ANSWER 5 OF 7 HCAPLUS COPYRIGHT 2003 ACS on STN
ACCESSION NUMBER: 1998:430094 HCAPLUS
DOCUMENT NUMBER: 129:90879
TITLE: Peptide ligands for the erythropoietin receptor
that act as erythropoietin agonists
INVENTOR(S): Wrighton, Nicholas C.; Dower, William J.; Chang,
Ray S.; Kashyap, Arun K.; Jolliffe, Linda K.;
Johnson, Dana; Mulcahy, Linda
PATENT ASSIGNEE(S): Affymax Technologies N.V., UK
SOURCE: U.S., 103 pp., Cont.-in-part of U. S. Ser. No.
155,940, abandoned.
CODEN: USXXAM
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 3
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 5773569	A	19980630	US 1995-484635	19950607
CA 2223833	AA	19961219	CA 1996-2223833	19960607
WO 9640749	A1	19961219	WO 1996-US9810	19960607
W: AL, AM, AT, AU, AZ, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG				
RW: KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA				
AU 9661667	A1	19961230	AU 1996-61667	19960607
AU 712713	B2	19991111		
CN 1192748	A	19980909	CN 1996-196094	19960607
EP 886648	A1	19981230	EP 1996-919296	19960607
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
JP 11507367	T2	19990629	JP 1996-502023	19960607
BR 9609006	A	19991214	BR 1996-9006	19960607
PL 185040	B1	20030228	PL 1996-323858	19960607
US 5986047	A	19991116	US 1997-827570	19970328
NO 9705729	A	19980205	NO 1997-5729	19971205
PRIORITY APPLN. INFO.:			US 1993-155940	B2 19931119
			US 1995-484631	A 19950607
			US 1995-484635	A 19950607
			WO 1996-US9810	W 19960607

OTHER SOURCE(S): MARPAT 129:90879
AB Peptides of 10 to 40 or more amino acids that bind and activate the
erythropoietin receptor (EPO-R) or otherwise act as an EPO agonist
for therapeutic uses are described. Peptides were identified by
screening of libraries prepared using degenerate oligonucleotides to
construct a phage display library that was screened by panning with
the receptor. Candidate peptides were synthesized as C-terminal
amide derivs by standard Fmoc on PAL resins and tested for biol.
activity. Many peptides showed greater affinity for the receptor
than did erythropoietin.

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IT 209594-31-0

RL: BAC (Biological activity or effector, except adverse); BSU
(Biological study, unclassified); PRP (Properties); BIOL (Biological
study)

(amino acid sequence; peptide ligands for erythropoietin receptor
that act as erythropoietin agonists)

REFERENCE COUNT: 27 THERE ARE 27 CITED REFERENCES AVAILABLE
FOR THIS RECORD. ALL CITATIONS AVAILABLE
IN THE RE FORMAT

L2 ANSWER 6 OF 7 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1998:129605 HCAPLUS

DOCUMENT NUMBER: 128:176424

TITLE: Identification of a 13 Amino Acid Peptide
Mimetic of Erythropoietin and Description of
Amino Acids Critical for the Mimetic Activity of
EMP1

AUTHOR(S): Johnson, Dana L.; Farrell, Francis X.; Barbone,
Francis P.; McMahon, Frank J.; Tullai, Jennifer;
Hoey, Kenway; Livnah, Oded; Wrighton, Nicholas
C.; Middleton, Steven A.; Loughney, Deborah A.;
Stura, Enrico A.; Dower, William J.; Mulcahy,
Linda S.; Wilson, Ian A.; Jolliffe, Linda K.

CORPORATE SOURCE: R. W. Johnson Pharmaceutical Research Institute
Drug Discovery Research, Raritan, NJ, 08869, USA

SOURCE: Biochemistry (1998), 37(11), 3699-3710
CODEN: BICHAW; ISSN: 0006-2960

PUBLISHER: American Chemical Society

DOCUMENT TYPE: Journal

LANGUAGE: English

AB To obtain information about the functional importance of amino acids
required for effective erythropoietin (EPO) mimetic action, the
conserved residues of a peptide mimetic of EPO, recently discovered
by phage display, were subjected to an alanine replacement strategy.
Further, to identify a minimal mimetic peptide sequence, a series of
truncation peptides has been generated. One EPO mimetic peptide
sequence, EMP1, was targeted and more than 25 derivs. of this
sequence were evaluated for their ability to compete with [125I]EPO
for receptor binding and for their ability to support the
proliferation of two EPO-responsive cell lines. Two hydrophobic
amino acids, Tyr4 and Trp13, appear essential for mimetic action,
and aromatic residues appear to be important at these sites. These
findings are consistent with the previously reported x-ray crystal
structure of EMP1 complexed with the extracellular domain of the EPO
receptor (EPO binding protein; EBP). In the authors' efforts to
define the structural elements required for EPO mimetic action, a 13
amino acid peptide was identified which possesses mimetic properties
and contains a minimal agonist epitope. The ability of this peptide
to effectively serve as a mimetic capable of the induction of
EPO-responsive cell proliferation appears to reside within a single
residue, equivalent to position Tyr4 to EMP1, when present in a sequence
that includes the cyclic core peptide structure. Although these
peptides are less potent than EPO, they should serve as an excellent
starting point for the design of compds. with EPO mimetic activity.

IT 203397-46-0

RL: BAC (Biological activity or effector, except adverse); BSU
(Biological study, unclassified); PRP (Properties); BIOL (Biological
study)

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(identification of a 13 amino acid peptide mimetic of erythropoietin and description of amino acids critical for mimetic activity)

REFERENCE COUNT: 25 THERE ARE 25 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 7 OF 7 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1997:148850 HCAPLUS

DOCUMENT NUMBER: 126:152802

TITLE: Linear, cyclic, and disulfide dimer synthetic peptides as erythropoietin agonists, binding by erythropoietin receptor, and pharmaceutical uses
INVENTOR(S): Wrighton, Nicholas C.; Dower, William J.; Chang, Ray S.; Kashyap, Arun K.; Jolliffe, Linda K.; Johnson, Dana; Mulcahy, Linda

PATENT ASSIGNEE(S): Johnson and Johnson Corporation, USA; Affymax Technologies, N.V.; Wrighton, Nicholas C.; Dower, William J.; Chang, Ray S.; Kashyap, Arun K.; Jolliffe, Linda K.; Johnson, Dana; Mulcahy, Linda

SOURCE: PCT Int. Appl., 94 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 3

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9640749	A1	19961219	WO 1996-US9810	19960607
W:	AL, AM, AT, AU, AZ, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG			
RW:	KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA			
US 5773569	A	19980630	US 1995-484635	19950607
US 5830851	A	19981103	US 1995-484631	19950607
AU 9661667	A1	19961230	AU 1996-61667	19960607
AU 712713	B2	19991111		
EP 886648	A1	19981230	EP 1996-919296	19960607
R:	AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI			
JP 11507367	T2	19990629	JP 1996-502023	19960607
BR 9609006	A	19991214	BR 1996-9006	19960607
PL 185040	B1	20030228	PL 1996-323858	19960607
NO 9705729	A	19980205	NO 1997-5729	19971205
PRIORITY APPLN. INFO.:			US 1995-484631	A 19950607
			US 1995-484635	A 19950607
			US 1993-155940	B2 19931119
			WO 1996-US9810	W 19960607

OTHER SOURCE(S): MARPAT 126:152802

AB This invention includes peptides of 10 to 40 or more amino acid residues in length and having the sequence X3X4X5GPX6TWX7X8 where each amino acid is indicated by standard one letter abbreviation; X3 is C; X4 is R, H, L, or W; X5 is M, F, or I; X6 is independently selected from any one of the 20 genetically coded L-amino acids; X7

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is D, E, I, L, or V; and X8is C, which bind and activate the erythropoietin receptor (EPO-R) or otherwise act as EPO agonists, and methods for their use. The peptides are mostly linear, or may be cyclic. Disulfide dimers are also included. These are useful for treating anemia, abnormal erythropoiesis, and other disease states.

IT **186526-47-6**

RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(erythropoietin agonist; linear, cyclic, and disulfide dimer synthetic peptides as erythropoietin agonists, binding by erythropoietin receptor, and pharmaceutical uses)

FILE 'HOME' ENTERED AT 12:26:26 ON 06 NOV 2003

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 5, 2003, 19:05:39 ; Search time 171 Seconds
(without alignments)
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 5728757 seqs, 909918778 residues

Total number of hits satisfying chosen parameters: 5728757

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Listing first 100 summaries

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24: /cgn2_6/ptodata/1/paa/US099A COMB.pep:*

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26: /cgn2_6/ptodata/1/paa/US100 COMB.pep:*

27: /cgn2_6/ptodata/1/paa/US101 COMB.pep:*

28: /cgn2_6/ptodata/1/paa/US102 COMB.pep:*

29: /cgn2_6/ptodata/1/paa/US103 COMB.pep:*

30: /cgn2_6/ptodata/1/paa/US104 COMB.pep:*

31: /cgn2_6/ptodata/1/paa/US106 COMB.pep:*

32: /cgn2_6/ptodata/1/paa/US60 COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	123	100.0	20	12	US-08-827-573-52 Sequence 52, Appl

2	123	100.0	20	15	US-09-155-158-52 Sequence 52, Appl
3	123	100.0	20	23	US-09-863-600E-19 Sequence 19, Appl
4	123	100.0	20	27	US-10-156-934-52 Sequence 52, Appl
5	119	96.7	20	12	US-08-827-573-189 Sequence 189, App
6	119	96.7	20	12	US-08-827-573-247 Sequence 247, App
7	119	96.7	20	12	US-08-827-573-248 Sequence 248, App
8	119	96.7	20	12	US-08-827-573-249 Sequence 249, App
9	119	96.7	20	12	US-08-827-573-250 Sequence 250, App
10	119	96.7	20	15	US-09-155-158-189 Sequence 189, App
11	119	96.7	20	15	US-09-155-158-247 Sequence 247, App
12	119	96.7	20	15	US-09-155-158-248 Sequence 248, App
13	119	96.7	20	15	US-09-155-158-249 Sequence 249, App
14	119	96.7	20	15	US-09-155-158-250 Sequence 250, App
15	119	96.7	20	23	US-09-863-600E-29 Sequence 29, Appl
16	119	96.7	20	23	US-09-863-600E-37 Sequence 37, Appl
17	119	96.7	20	23	US-09-863-600E-38 Sequence 38, Appl
18	119	96.7	20	23	US-09-863-600E-39 Sequence 39, Appl
19	119	96.7	20	23	US-09-863-600E-40 Sequence 40, Appl
20	119	96.7	20	23	US-09-863-600E-41 Sequence 41, Appl
21	119	96.7	20	23	US-09-863-600E-42 Sequence 42, Appl
22	119	96.7	20	27	US-10-156-934-189 Sequence 189, App
23	119	96.7	20	27	US-10-156-934-247 Sequence 247, App
24	119	96.7	20	27	US-10-156-934-248 Sequence 248, App
25	119	96.7	20	27	US-10-156-934-249 Sequence 249, App
26	119	96.7	20	27	US-10-156-934-250 Sequence 250, App
27	117	95.1	20	1	PCT-US02-27637-11 Sequence 11, Appl
28	117	95.1	20	1	PCT-US02-27637-25 Sequence 25, Appl
29	117	95.1	20	1	PCT-US03-18645-7 Sequence 7, Appl
30	117	95.1	20	1	PCT-US99-25044-87 Sequence 87, Appl
31	117	95.1	20	1	PCT-US99-25044-1025 Sequence 1025, Ap
32	117	95.1	20	5	US-08-155-940A-8 Sequence 8, Appl
33	117	95.1	20	5	US-08-155-940A-35 Sequence 35, Appl
34	117	95.1	20	5	US-08-155-940A-49 Sequence 49, Appl
35	117	95.1	20	8	US-08-451-550-8 Sequence 8, Appl
36	117	95.1	20	8	US-08-451-550-35 Sequence 35, Appl
37	117	95.1	20	8	US-08-451-550-49 Sequence 49, Appl
38	117	95.1	20	12	US-08-827-573-8 Sequence 8, Appl
39	117	95.1	20	12	US-08-827-573-190 Sequence 190, App
40	117	95.1	20	14	US-09-052-889-34 Sequence 34, Appl
41	117	95.1	20	15	US-09-155-158-8 Sequence 8, Appl
42	117	95.1	20	15	US-09-155-158-190 Sequence 190, App
43	117	95.1	20	17	US-09-341-590-117 Sequence 117, App
44	117	95.1	20	18	US-09-428-082-87 Sequence 87, Appl
45	117	95.1	20	18	US-09-428-082-1025 Sequence 1025, Ap
46	117	95.1	20	18	US-09-428-082B-87 Sequence 87, Appl
47	117	95.1	20	18	US-09-428-082B-93 Sequence 93, Appl
48	117	95.1	20	18	US-09-428-082B-1025 Sequence 1025, Ap
49	117	95.1	20	19	US-09-563-286B-87 Sequence 87, Appl
50	117	95.1	20	19	US-09-563-286B-93 Sequence 93, Appl
51	117	95.1	20	19	US-09-563-286C-87 Sequence 87, Appl
52	117	95.1	20	19	US-09-563-286C-93 Sequence 93, Appl
53	117	95.1	20	19	US-09-563-286C-1025 Sequence 1025, Ap
54	117	95.1	20	21	US-09-723-547-34 Sequence 34, Appl
55	117	95.1	20	21	US-09-723-873-34 Sequence 34, Appl
56	117	95.1	20	21	US-09-723-890-34 Sequence 34, Appl
57	117	95.1	20	21	US-09-723-891-34 Sequence 34, Appl
58	117	95.1	20	21	US-09-723-901-34 Sequence 34, Appl
59	117	95.1	20	21	US-09-723-912-34 Sequence 34, Appl
60	117	95.1	20	21	US-09-723-913-34 Sequence 34, Appl
61	117	95.1	20	21	US-09-723-931-34 Sequence 34, Appl
62	117	95.1	20	21	US-09-724-062-34 Sequence 34, Appl
63	117	95.1	20	21	US-09-724-065-34 Sequence 34, Appl
64	117	95.1	20	21	US-09-724-095-34 Sequence 34, Appl
65	117	95.1	20	21	US-09-724-114-34 Sequence 34, Appl
66	117	95.1	20	21	US-09-724-127-34 Sequence 34, Appl
67	117	95.1	20	21	US-09-724-157-34 Sequence 34, Appl
68	117	95.1	20	21	US-09-724-481-34 Sequence 34, Appl
69	117	95.1	20	23	US-09-858-935B-66 Sequence 66, Appl
70	117	95.1	20	23	US-09-863-600B-8 Sequence 8, Appl
71	117	95.1	20	23	US-09-863-600E-30 Sequence 30, Appl
72	117	95.1	20	26	US-10-028-564-1 Sequence 1, Appl
73	117	95.1	20		
74	117	95.1	20		

75 117 95.1 20 27 US-10-156-934-8 Sequence 8, Appli
76 117 95.1 20 27 US-10-156-934-190 Sequence 190, Appl
77 117 95.1 20 28 US-10-231-494-11 Sequence 11, Appl
78 117 95.1 20 28 US-10-231-494-25 Sequence 25, Appl
79 117 95.1 20 28 US-10-271-869-66 Sequence 66, Appl
80 117 95.1 20 29 US-10-378-094-11 Sequence 11, Appl
81 117 95.1 20 31 US-10-609-217-87 Sequence 87, Appl
82 117 95.1 20 31 US-10-609-217-93 Sequence 93, Appl
83 117 95.1 20 31 US-10-609-217-1025 Sequence 1025, Ap
84 117 95.1 20 31 US-10-645-761-87 Sequence 87, Appl
85 117 95.1 20 31 US-10-645-761-93 Sequence 93, Appl
86 117 95.1 20 31 US-10-645-761-1025 Sequence 1025, Ap
87 117 95.1 20 32 US-60-460-829-11 Sequence 11, Appl
88 117 95.1 22 1 PCT-US99-25044-97 Sequence 97, Appl
89 117 95.1 22 18 US-09-428-082-97 Sequence 97, Appl
90 117 95.1 22 18 US-09-428-082B-97 Sequence 97, Appl
91 117 95.1 22 19 US-09-563-286B-97 Sequence 97, Appl
92 117 95.1 22 19 US-09-563-286C-97 Sequence 97, Appl
93 117 95.1 22 31 US-10-609-217-97 Sequence 97, Appl
94 117 95.1 22 31 US-10-645-761-97 Sequence 97, Appl
95 117 95.1 23 1 PCT-US99-25044-94 Sequence 94, Appl
96 117 95.1 23 1 PCT-US99-25044-98 Sequence 98, Appl
97 117 95.1 23 12 US-08-827-573-20 Sequence 20, Appl
98 117 95.1 23 15 US-09-155-158-20 Sequence 20, Appl
99 117 95.1 23 18 US-09-428-082-94 Sequence 94, Appl
100 117 95.1 23 18 US-09-428-082-98 Sequence 98, Appl

ALIGNMENTS

RESULT 1
US-09-827-573-52
; Sequence 52, Application US/08827573
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/827.573
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,635
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-1
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043

; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-827-573-52
Query Match 100.0%; Score 123; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.9e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTASCHFGPLTWCKPQGG 20
RESULT 2
US-09-155-158-52
; Sequence 52, Application US/09155158
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 262
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Affymax Research Institute
; STREET: 4001 Miranda Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,158
; FILING DATE: 03-Jun-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/09810
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: US 08/484,635
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/484,631
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Stracker, Elaine C.
; REGISTRATION NUMBER: 43,166
; REFERENCE/DOCKET NUMBER: 1053.3W
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 812-8700
; TELEFAX: (650) 424-0832
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 52:
US-09-155-158-52

Query Match 100.0%; Score 123; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.9e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
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Db 1 GGTASCHFGPLTWCKPQGG 20

RESULT 3

US-09-863-600E-19

; Sequence 19, Application US/09863600E

; GENERAL INFORMATION:

; APPLICANT: Smith-Swintosky, Virginia

; APPLICANT: Renzi, Michael

; APPLICANT: Plata-Salaman, Carlos

; APPLICANT: Jolliffe, Linda

; APPLICANT: Farrell, Francis

; APPLICANT: Johnson, Dana

; TITLE OF INVENTION: Neuroprotective Peptides

; FILE REFERENCE: PRI-0014 (ORT-1436)

; CURRENT APPLICATION NUMBER: US/09/863,600E

; CURRENT FILING DATE: 2001-05-23

; PRIOR APPLICATION NUMBER: 60/207,654

; PRIOR FILING DATE: 2000-05-26

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 19

; LENGTH: 20

; TYPE: PPT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic Peptide

US-09-863-600E-19

Query Match 100.0%; Score 123; DB 23; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.9e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
|||||
Db 1 GGTASCHFGPLTWCKPQGG 20

RESULT 4

US-10-156-934-52

; Sequence 52, Application US/10156934

; GENERAL INFORMATION:

; APPLICANT: Wrighton, Nicholas C.

; Dower, William J.

; Chang, Ray S.

; Kashyap, Arun K.

; TITLE OF INVENTION: Compounds and Peptides That Bind to the

; Erythropoietin Receptor

; NUMBER OF SEQUENCES: 267

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Affymax Research Institute

; STREET: 4001 Miranda Avenue

; CITY: Palo Alto

; STATE: California

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/156,934

; FILING DATE: 28-May-2002

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 09/155,158
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: PCT/US96/09810
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: US 08/484,635
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/484,631
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993

ATTORNEY/AGENT INFORMATION:

NAME: Hostetler, Michael J.

REGISTRATION NUMBER: 47,664

REFERENCE/DOCKET NUMBER: 033134.1053.CIP4

TELECOMMUNICATION INFORMATION:

TELEPHONE: (858) 720-2500

TELEFAX: (858) 720-3700

INFORMATION FOR SEQ ID NO: 52:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 52:

US-10-156-934-52

Query Match 100.0%; Score 123; DB 27; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.9e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
|||||
Db 1 GGTASCHFGPLTWCKPQGG 20

RESULT 5

US-08-827-573-189

; Sequence 189, Application US/08827573

; GENERAL INFORMATION:

; APPLICANT: Wrighton, Nicholas C.

; APPLICANT: Dower, William J.

; APPLICANT: Chang, Ray S.

; APPLICANT: Kashyap, Arun K.

; APPLICANT: Jolliffe, Linda K.

; APPLICANT: Johnson, Dana

; APPLICANT: Mulcahy, Linda

; TITLE OF INVENTION: Compounds and Peptides That Bind to the

; Erythropoietin Receptor

; NUMBER OF SEQUENCES: 259

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew

; STREET: One Market Plaza, Steuart Street Tower

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94105-1492

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/827,573

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/484,635

; FILING DATE: 07-JUN-1995

; APPLICATION NUMBER: US 08/155,940

; FILING DATE: 19-NOV-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Garrett-Wackowski, Eugenia

REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 16528A-43-1-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 189:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-827-573-189

Query Match 96.7%; Score 119; DB 12; Length 20;
Best Local Similarity 95.0%; Pred. No. 2.6e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
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DB 1 GGITSCHEGPLTWCKPQGG 20

RESULT 6

US-08-827-573-247
; Sequence 247, Application US/08827573
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/827,573
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,635
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 247:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:

NAME/KEY: Modified-site
LOCATION: 4
OTHER INFORMATION: /product= "OTHER"
OTHER INFORMATION: /note= "Xaa = para-nitro-phenylalanine"
US-08-827-573-247

Query Match 96.7%; Score 119; DB 12; Length 20;
Best Local Similarity 95.0%; Pred. No. 2.6e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
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DB 1 GGTXSCHFGPLTWCKPQGG 20

RESULT 7

US-08-827-573-248
; Sequence 248, Application US/08827573
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/827,573
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,635
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 248:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /product= "OTHER"
; OTHER INFORMATION: /note= "Xaa = para-amino-phenylalanine"
US-08-827-573-248

Query Match 96.7%; Score 119; DB 12; Length 20;
Best Local Similarity 95.0%; Pred. No. 2.6e-09;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
 ||| |||||
 Db 1 GGTXSCHFGPLTWCKPQGG 20

RESULT 8

US-08-827-573-249
 ; Sequence 249, Application US/08827573
 ; GENERAL INFORMATION:
 ; APPLICANT: Wrighton, Nicholas C.
 ; APPLICANT: Dower, William J.
 ; APPLICANT: Chang, Ray S.
 ; APPLICANT: Kashyap, Arun K.
 ; APPLICANT: Jolliffe, Linda K.
 ; APPLICANT: Johnson, Dana
 ; APPLICANT: Mulcahy, Linda
 ; TITLE OF INVENTION: Compounds and Peptides That Bind to the
 ; Erythropoietin Receptor
 ; NUMBER OF SEQUENCES: 259
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew
 ; STREET: One Market Plaza, Steuart Street Tower
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94105-1492
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/827,573
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/484,635
 ; FILING DATE: 07-JUN-1995
 ; APPLICATION NUMBER: US 08/155,940
 ; FILING DATE: 19-NOV-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Garrett-Wackowski, Eugenia
 ; REGISTRATION NUMBER: 37,330
 ; REFERENCE/DOCKET NUMBER: 16528A-43-1-1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 543-9600
 ; TELEFAX: (415) 543-5043
 ; INFORMATION FOR SEQ ID NO: 249:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 20 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; FEATURE:
 ; NAME/KEY: Modified-site
 ; LOCATION: 4
 ; OTHER INFORMATION: /product= "OTHER"
 ; OTHER INFORMATION: /note= "Xaa = para-fluoro-phenylalanine"

US-08-827-573-249
 Query Match 96.7%; Score 119; DB 12; Length 20;
 Best Local Similarity 95.0%; Pred. No. 2.6e-09;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GGTASCHFGPLTWCKPQGG 20
 ||| |||||
 Db 1 GGTXSCHFGPLTWCKPQGG 20

RESULT 9

US-08-827-573-250
 ; Sequence 250, Application US/08827573
 ; GENERAL INFORMATION:
 ; APPLICANT: Wrighton, Nicholas C.
 ; APPLICANT: Dower, William J.
 ; APPLICANT: Chang, Ray S.
 ; APPLICANT: Kashyap, Arun K.
 ; APPLICANT: Jolliffe, Linda K.
 ; APPLICANT: Johnson, Dana
 ; APPLICANT: Mulcahy, Linda
 ; TITLE OF INVENTION: Compounds and Peptides That Bind to the
 ; Erythropoietin Receptor
 ; NUMBER OF SEQUENCES: 259
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew
 ; STREET: One Market Plaza, Steuart Street Tower
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94105-1492
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/827,573
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/484,635
 ; FILING DATE: 07-JUN-1995
 ; APPLICATION NUMBER: US 08/155,940
 ; FILING DATE: 19-NOV-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Garrett-Wackowski, Eugenia
 ; REGISTRATION NUMBER: 37,330
 ; REFERENCE/DOCKET NUMBER: 16528A-43-1-1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 543-9600
 ; TELEFAX: (415) 543-5043
 ; INFORMATION FOR SEQ ID NO: 250:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 20 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; FEATURE:
 ; NAME/KEY: Modified-site
 ; LOCATION: 4
 ; OTHER INFORMATION: /product= "OTHER"
 ; OTHER INFORMATION: /note= "Xaa = 3,5-dibromo-tyrosine"

US-08-827-573-250
 Query Match 96.7%; Score 119; DB 12; Length 20;
 Best Local Similarity 95.0%; Pred. No. 2.6e-09;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GGTASCHFGPLTWCKPQGG 20
 ||| |||||
 Db 1 GGTXSCHFGPLTWCKPQGG 20

RESULT 10

US-09-155-158-189
 ; Sequence 189, Application US/09155158
 ; GENERAL INFORMATION:
 ; APPLICANT: Wrighton, Nicholas C.
 ; APPLICANT: Dower, William J.
 ; APPLICANT: Chang, Ray S.
 ; APPLICANT: Kashyap, Arun K.
 ; APPLICANT: Jolliffe, Linda K.

```

;
; Johnson, Dana
; Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; Erythropoietin Receptor
;
; NUMBER OF SEQUENCES: 262
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Affymax Research Institute
; STREET: 4001 Miranda Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,158
; FILING DATE: 03-Jun-1999
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/09810
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: US 08/484,635
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/484,631
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Stracker, Elaine C.
; REGISTRATION NUMBER: 43,166
; REFERENCE/DOCKET NUMBER: 1053.3W
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 812-8700
; TELEFAX: (650) 424-0832
;
; INFORMATION FOR SEQ ID NO: 189:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /product= "OTHER"
; /note= "Xaa = para-nitro-phenylalanine"
; SEQUENCE DESCRIPTION: SEQ ID NO: 189:
US-09-155-158-189

Query Match 96.7%; Score 119; DB 15; Length 20;
Best Local Similarity 95.0%; Pred. No. 2.6e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTTSCHFGPLTWCKPQGG 20

RESULT 11
US-09-155-158-247
; Sequence 247, Application US/09155158
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; Dower, William J.
; Chang, Ray S.
; Kashyap, Arun K.
; Jolliffe, Linda K.
; Johnson, Dana
; Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; Erythropoietin Receptor
; NUMBER OF SEQUENCES: 262
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Affymax Research Institute
; STREET: 4001 Miranda Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA

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;
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,158
; FILING DATE: 03-Jun-1999
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/09810
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: US 08/484,635
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/484,631
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Stracker, Elaine C.
; REGISTRATION NUMBER: 43,166
; REFERENCE/DOCKET NUMBER: 1053.3W
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 812-8700
; TELEFAX: (650) 424-0832
;
; INFORMATION FOR SEQ ID NO: 247:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /product= "OTHER"
; /note= "Xaa = para-nitro-phenylalanine"
; SEQUENCE DESCRIPTION: SEQ ID NO: 247:
US-09-155-158-247

Query Match 96.7%; Score 119; DB 15; Length 20;
Best Local Similarity 95.0%; Pred. No. 2.6e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTXSCHFGPLTWCKPQGG 20

RESULT 12
US-09-155-158-248
; Sequence 248, Application US/09155158
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; Dower, William J.
; Chang, Ray S.
; Kashyap, Arun K.
; Jolliffe, Linda K.
; Johnson, Dana
; Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; Erythropoietin Receptor
; NUMBER OF SEQUENCES: 262
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Affymax Research Institute
; STREET: 4001 Miranda Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA

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;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/155.158
;; FILING DATE: 03-Jun-1999
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US96/09810
;; FILING DATE: 07-JUN-1996
;; APPLICATION NUMBER: US 08/484,635
;; FILING DATE: 07-JUN-1995
;; APPLICATION NUMBER: US 08/484,631
;; FILING DATE: 07-JUN-1995
;; APPLICATION NUMBER: US 08/155,940
;; FILING DATE: 19-NOV-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Stracker, Elaine C.
;; REGISTRATION NUMBER: 43,166
;; REFERENCE/DOCKET NUMBER: 1053.3W
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (650) 812-8700
;; TELEFAX: (650) 424-0832
;; INFORMATION FOR SEQ ID NO: 250:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 20 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: <Unknown>
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; FEATURE:
;; NAME/KEY: Modified-site
;; LOCATION: 4
;; OTHER INFORMATION: /product= "OTHER"
;; /note= "Xaa = 3,5-dibromo-tyrosine"
;; SEQUENCE DESCRIPTION: SEQ ID NO: 250:
US-09-155-158-250

Query Match 96.7%; Score 119; DB 15; Length 20;
Best Local Similarity 95.0%; Pred. No. 2.6e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
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Db 1 GGTXSCHFGPLTWCKPQGG 20

RESULT 15
US-09-863-600E-29
; Sequence 29, Application US/09863600E
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-09-863-600E-29

Query Match 96.7%; Score 119; DB 23; Length 20;
Best Local Similarity 95.0%; Pred. No. 2.6e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| ||||| |||||
Db 1 GGTTSCHFGPLTWCKPQGG 20

RESULT 16
US-09-863-600E-37
; Sequence 37, Application US/09863600E
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 37
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
; NAME/KEY: misc feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: Xaa is D-Tyr
US-09-863-600E-37

Query Match 96.7%; Score 119; DB 23; Length 20;
Best Local Similarity 95.0%; Pred. No. 2.6e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| ||||| |||||
Db 1 GGTXSCHFGPLTWCKPQGG 20

RESULT 17
US-09-863-600E-38
; Sequence 38, Application US/09863600E
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
; NAME/KEY: misc feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: Xaa is p-NO2-Phe
US-09-863-600E-38

US-09-863-600E-38

Query Match 96.7%; Score 119; DB 23; Length 20;
Best Local Similarity 95.0%; Pred. No. 2.6e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTASCHFGPLTWCKPQGG 20

RESULT 18
US-09-863-600E-39
; Sequence 39, Application US/09863600E
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 39
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Synthetic Peptide
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: Xaa is p-NH2-Phe
US-09-863-600E-39

Query Match 96.7%; Score 119; DB 23; Length 20;
Best Local Similarity 95.0%; Pred. No. 2.6e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTASCHFGPLTWCKPQGG 20

RESULT 19
US-09-863-600E-40
; Sequence 40, Application US/09863600E
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Synthetic Peptide
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: Xaa is p-F-Phe
US-09-863-600E-40

Query Match 96.7%; Score 119; DB 23; Length 20;
Best Local Similarity 95.0%; Pred. No. 2.6e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTASCHFGPLTWCKPQGG 20

RESULT 20
US-09-863-600E-41
; Sequence 41, Application US/09863600E
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 41
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Synthetic Peptide
; FEATURE:
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: Xaa is p-I-Phe
US-09-863-600E-41

Query Match 96.7%; Score 119; DB 23; Length 20;
Best Local Similarity 95.0%; Pred. No. 2.6e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTASCHFGPLTWCKPQGG 20

RESULT 21
US-09-863-600E-42
; Sequence 42, Application US/09863600E
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2

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; SEQ ID NO 42
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: Xaa is 3,5-dibromo-Tyr
US-09-863-600E-42

Query Match          96.7%; Score 119; DB 23; Length 20;
Best Local Similarity 95.0%; Pred. No. 2.6e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
   ||| ||||| ||||| |||||
DB 1 GGTXSCHFGPLTWCKPQGG 20

RESULT 22
US-10-156-934-189
; Sequence 189, Application US/10156934
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; Dower, William J.
; Chang, Ray S.
; Kashyap, Arun K.
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; Erythropoietin Receptor
; NUMBER OF SEQUENCES: 267
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Affymax Research Institute
; STREET: 4001 Miranda Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/156,934
; FILING DATE: 28-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/155,158
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: PCT/US96/09810
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: US 08/484,635
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/484,631
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Hostetler, Michael J.
; REGISTRATION NUMBER: 47,664
; REFERENCE/DOCKET NUMBER: 033134.1053.CIP4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (858) 720-2500
; TELEFAX: (858) 720-3700
; INFORMATION FOR SEQ ID NO: 189:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
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; SEQUENCE DESCRIPTION: SEQ ID NO: 189:
US-10-156-934-189

Query Match          96.7%; Score 119; DB 27; Length 20;
Best Local Similarity 95.0%; Pred. No. 2.6e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
   ||| ||||| ||||| |||||
DB 1 GGTTSCHFGPLTWCKPQGG 20

RESULT 23
US-10-156-934-247
; Sequence 247, Application US/10156934
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; Dower, William J.
; Chang, Ray S.
; Kashyap, Arun K.
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; Erythropoietin Receptor
; NUMBER OF SEQUENCES: 267
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Affymax Research Institute
; STREET: 4001 Miranda Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/156,934
; FILING DATE: 28-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/155,158
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: PCT/US96/09810
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: US 08/484,635
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/484,631
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Hostetler, Michael J.
; REGISTRATION NUMBER: 47,664
; REFERENCE/DOCKET NUMBER: 033134.1053.CIP4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (858) 720-2500
; TELEFAX: (858) 720-3700
; INFORMATION FOR SEQ ID NO: 247:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /product= "OTHER"
; /note= "Xaa = para-nitro-phenylalanine"
; SEQUENCE DESCRIPTION: SEQ ID NO: 247:
US-10-156-934-247

Query Match          96.7%; Score 119; DB 27; Length 20;
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Best Local Similarity 95.0%; Pred. No. 2.6e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTASCHFGPLTWCKPQGG 20

RESULT 24
US-10-156-934-248
; Sequence 248, Application US/10156934
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; Dower, William J.
; Chang, Ray S.
; Kashyap, Arun K.
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; Erythropoietin Receptor
; NUMBER OF SEQUENCES: 267
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Affymax Research Institute
; STREET: 4001 Miranda Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/156,934
; FILING DATE: 28-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/155,158
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: PCT/US96/09810
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: US 08/484,635
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/484,631
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Hostetler, Michael J.
; REGISTRATION NUMBER: 47,664
; REFERENCE/DOCKET NUMBER: 033134.1053.CIP4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (858) 720-2500
; TELEFAX: (858) 720-3700
; INFORMATION FOR SEQ ID NO: 248:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /product= "OTHER"
; /note= "Xaa = para-amino-phenylalanine"
; SEQUENCE DESCRIPTION: SEQ ID NO: 248:
US-10-156-934-248

Query Match 96.7%; Score 119; DB 27; Length 20;
Best Local Similarity 95.0%; Pred. No. 2.6e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20

Db 1 GGTASCHFGPLTWCKPQGG 20

RESULT 25
US-10-156-934-249
; Sequence 249, Application US/10156934
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; Dower, William J.
; Chang, Ray S.
; Kashyap, Arun K.
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; Erythropoietin Receptor
; NUMBER OF SEQUENCES: 267
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Affymax Research Institute
; STREET: 4001 Miranda Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/156,934
; FILING DATE: 28-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/155,158
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: PCT/US96/09810
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: US 08/484,635
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/484,631
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Hostetler, Michael J.
; REGISTRATION NUMBER: 47,664
; REFERENCE/DOCKET NUMBER: 033134.1053.CIP4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (858) 720-2500
; TELEFAX: (858) 720-3700
; INFORMATION FOR SEQ ID NO: 249:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /product= "OTHER"
; /note= "Xaa = para-fluoro-phenylalanine"
; SEQUENCE DESCRIPTION: SEQ ID NO: 249:
US-10-156-934-249

Query Match 96.7%; Score 119; DB 27; Length 20;
Best Local Similarity 95.0%; Pred. No. 2.6e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTASCHFGPLTWCKPQGG 20

RESULT 26
US-10-156-934-250
; Sequence 250, Application US/10156934
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; Dower, William J.
; Chang, Ray S.
; Kashyap, Arun K.
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; Erythropoietin Receptor
; NUMBER OF SEQUENCES: 267
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Affymax Research Institute
; STREET: 4001 Miranda Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/156,934
; FILING DATE: 28-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/155,158
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: PCT/US96/09810
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: US 08/484,635
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/484,631
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Hostetler, Michael J.
; REGISTRATION NUMBER: 47,664
; REFERENCE/DOCKET NUMBER: 033134.1053.CIP4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (858) 720-2500
; TELEFAX: (858) 720-3700
; INFORMATION FOR SEQ ID NO: 250:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /product= "OTHER"
; /note= "Xaa = 3,5-dibromo-tyrosine"
; SEQUENCE DESCRIPTION: SEQ ID NO: 250:
US-10-156-934-250
Query Match 96.7%; Score 119; DB 27; Length 20;
Best Local Similarity 95.0%; Pred. No. 2.6e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTXSCHFGPLTWCKPQGG 20
RESULT 27
PCT-US02-27637-11
; Sequence 11, Application PC/TUS0227637
; GENERAL INFORMATION:

; APPLICANT: Prior, Christopher P.
; TITLE OF INVENTION: Modified Transferrin Fusion Proteins
; FILE REFERENCE: 54710-5001-WO
; CURRENT APPLICATION NUMBER: PCT/US02/27637
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/315,745
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/334,059
; PRIOR FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: EPO mimetic
; OTHER INFORMATION: peptide
PCT-US02-27637-11
Query Match 95.1%; Score 117; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 5e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTYSCHFGPLTWCKPQGG 20
RESULT 28
PCT-US02-27637-25
; Sequence 25, Application PC/TUS0227637
; GENERAL INFORMATION:
; APPLICANT: Prior, Christopher P.
; TITLE OF INVENTION: Modified Transferrin Fusion Proteins
; FILE REFERENCE: 54710-5001-WO
; CURRENT APPLICATION NUMBER: PCT/US02/27637
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/315,745
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/334,059
; PRIOR FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: EPO mimetic
; OTHER INFORMATION: sequences
PCT-US02-27637-25
Query Match 95.1%; Score 117; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 5e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTYSCHFGPLTWCKPQGG 20
RESULT 29
PCT-US03-18645-7
; Sequence 7, Application PC/TUS0318645
; GENERAL INFORMATION:
; APPLICANT: The Burnham Institute
; APPLICANT: Digicaylioglu, Murat
; APPLICANT: Lipton, Stuart A.
; TITLE OF INVENTION: Neuroprotective Synergy of
; Erythropoietin and Insulin-Like Growth Factors
; FILE REFERENCE: 66821-216
; CURRENT APPLICATION NUMBER: PCT/US03/18645

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; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: US 60/388,058
; PRIOR FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: US 60/458,145
; PRIOR FILING DATE: 2003-03-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
PCT-US03-18645-7

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```

Query Match          95.1%; Score 117; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 5e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      1 GGTASCHFGPLTWCKPQGG 20
      ||| ||||| ||||| |||||
Db      1 GGTYSCHFGPLTWCKPQGG 20

```

```

RESULT 30
PCT-US99-25044-87
; Sequence 87, Application PC/TUS9925044
; GENERAL INFORMATION:
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: FEIGE, ULRICH
; APPLICANT: CHEETHAM, JANET
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: PCT/US99/25044
; CURRENT FILING DATE: 1999-10-25
; EARLIER APPLICATION NUMBER: 60/105,371
; EARLIER FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 87
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:EPO-MIMETIC
PCT-US99-25044-87

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```

Query Match          95.1%; Score 117; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 5e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

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QY      1 GGTASCHFGPLTWCKPQGG 20
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Db      1 GGTYSCHFGPLTWCKPQGG 20

```

```

RESULT 31
PCT-US99-25044-1025
; Sequence 1025, Application PC/TUS9925044
; GENERAL INFORMATION:
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: FEIGE, ULRICH
; APPLICANT: CHEETHAM, JANET
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: PCT/US99/25044
; CURRENT FILING DATE: 1999-10-25
; EARLIER APPLICATION NUMBER: 60/105,371
; EARLIER FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133

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```

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1025
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:EPO MIMETIC
; OTHER INFORMATION: PEPTIDE
PCT-US99-25044-1025

```

```

Query Match          95.1%; Score 117; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 5e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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```

QY      1 GGTASCHFGPLTWCKPQGG 20
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Db      1 GGTYSCHFGPLTWCKPQGG 20

```

```

RESULT 32
US-08-155-940A-8
; Sequence 8, Application US/08155940A
; GENERAL INFORMATION:
; APPLICANT: Chang, Ray S.
; APPLICANT: Dower, William J.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Wrighton, Nicholas C.
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Affymax Technologies N.V., Administrative Offices
; STREET: 4001 Miranda Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/155,940A
; FILING DATE: 19-NOV-1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Stevens, Lauren L.
; REGISTRATION NUMBER: 36,691
; REFERENCE/DOCKET NUMBER: 11509-122/1053
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-496-2300
; TELEFAX: 415-424-0832
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-155-940A-8

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```

Query Match          95.1%; Score 117; DB 5; Length 20;
Best Local Similarity 95.0%; Pred. No. 5e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      1 GGTASCHFGPLTWCKPQGG 20
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Db      1 GGTYSCHFGPLTWCKPQGG 20

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RESULT 33
US-08-155-940A-35

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; Sequence 35, Application US/08155940A
; GENERAL INFORMATION:
; APPLICANT: Chang, Ray S.
; APPLICANT: Dower, William J.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Wrighton, Nicholas C.
; TITLE OF INVENTION: Compounds and peptides that bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Affymax Technologies N.V., Administrative Offices
; STREET: 4001 Miranda Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/155,940A
; FILING DATE: 19-NOV-1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Stevens, Lauren L.
; REGISTRATION NUMBER: 36,691
; REFERENCE/DOCKET NUMBER: 11509-122/1053
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-496-2300
; TELEFAX: 415-424-0832
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-155-940A-35

Query Match 95.1%; Score 117; DB 5; Length 20;
Best Local Similarity 95.0%; Pred. No. 5e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
   ||| ||||| ||||| |||||
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 34
US-08-155-940A-49
; Sequence 49, Application US/08155940A
; GENERAL INFORMATION:
; APPLICANT: Chang, Ray S.
; APPLICANT: Dower, William J.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Wrighton, Nicholas C.
; TITLE OF INVENTION: Compounds and peptides that bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Affymax Technologies N.V., Administrative Offices
; STREET: 4001 Miranda Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/155,940A
; FILING DATE: 19-NOV-1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Stevens, Lauren L.
; REGISTRATION NUMBER: 36,691
; REFERENCE/DOCKET NUMBER: 11509-122/1053
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-496-2300
; TELEFAX: 415-424-0832
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-155-940A-49

Query Match 95.1%; Score 117; DB 5; Length 20;
Best Local Similarity 95.0%; Pred. No. 5e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
   ||| ||||| ||||| |||||
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 35
US-08-451-550-8
; Sequence 8, Application US/08451550
; GENERAL INFORMATION:
; APPLICANT: Chang, Ray S.
; APPLICANT: Dower, William J.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Wrighton, Nicholas C.
; TITLE OF INVENTION: Compounds and peptides that bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Affymax Technologies N.V., Administrative Offices
; STREET: 4001 Miranda Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/451,550
; FILING DATE: Herewith
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Stevens, Lauren L.
; REGISTRATION NUMBER: 36,691
; REFERENCE/DOCKET NUMBER: 11509-122/1053
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-496-2300
; TELEFAX: 415-424-0832
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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; MOLECULE TYPE: peptide
US-08-451-550-8

Query Match          95.1%; Score 117; DB 8; Length 20;
Best Local Similarity 95.0%; Pred. No. 5e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GGTASCHFGPLTWCKPQGG 20
      ||| ||||| ||||| ||||| |||||
Db      1 GGTYSCHFGPLTWCKPQGG 20

RESULT 36
US-08-451-550-35
; Sequence 35, Application US/08451550
; GENERAL INFORMATION:
; APPLICANT: Chang, Ray S.
; APPLICANT: Dower, William J.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Wrighton, Nicholas C.
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Affymax Technologies N.V., Administrative Offices
; STREET: 4001 Miranda Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/451,550
; FILING DATE: Herewith
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Stevens, Lauren L.
; REGISTRATION NUMBER: 36,691
; REFERENCE/DOCKET NUMBER: 11509-122/1053
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-496-2300
; TELEFAX: 415-424-0832
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-451-550-35

Query Match          95.1%; Score 117; DB 8; Length 20;
Best Local Similarity 95.0%; Pred. No. 5e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GGTASCHFGPLTWCKPQGG 20
      ||| ||||| ||||| ||||| |||||
Db      1 GGTYSCHFGPLTWCKPQGG 20

RESULT 37
US-08-451-550-49
; Sequence 49, Application US/08451550
; GENERAL INFORMATION:
; APPLICANT: Chang, Ray S.
; APPLICANT: Dower, William J.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Wrighton, Nicholas C.
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Affymax Technologies N.V., Administrative Offices
; STREET: 4001 Miranda Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/451,550
; FILING DATE: Herewith
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Stevens, Lauren L.
; REGISTRATION NUMBER: 36,691
; REFERENCE/DOCKET NUMBER: 11509-122/1053
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-496-2300
; TELEFAX: 415-424-0832
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-451-550-35

Query Match          95.1%; Score 117; DB 8; Length 20;
Best Local Similarity 95.0%; Pred. No. 5e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GGTASCHFGPLTWCKPQGG 20
      ||| ||||| ||||| ||||| |||||
Db      1 GGTYSCHFGPLTWCKPQGG 20

RESULT 38
US-08-827-573-8
; Sequence 8, Application US/08827573
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; APPLICANT: Dower, William J.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Wrighton, Nicholas C.
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Affymax Technologies N.V., Administrative Offices
; STREET: 4001 Miranda Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/451,550
; FILING DATE: Herewith
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Stevens, Lauren L.
; REGISTRATION NUMBER: 36,691
; REFERENCE/DOCKET NUMBER: 11509-122/1053
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-496-2300
; TELEFAX: 415-424-0832
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-451-550-49

Query Match          95.1%; Score 117; DB 8; Length 20;
Best Local Similarity 95.0%; Pred. No. 5e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GGTASCHFGPLTWCKPQGG 20
      ||| ||||| ||||| ||||| |||||
Db      1 GGTYSCHFGPLTWCKPQGG 20
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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/827,573
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,635
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-1
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-827-573-8

Query Match 95.1%; Score 117; DB 12; Length 20;
Best Local Similarity 95.0%; Pred. No. 5e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
   ||| ||||| ||||| |||||
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 39
US-08-827-573-190
; Sequence 190, Application US/08827573
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/827,573
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,635
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
```

```
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 190:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-827-573-190

Query Match 95.1%; Score 117; DB 12; Length 20;
Best Local Similarity 95.0%; Pred. No. 5e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
   ||| ||||| ||||| |||||
Db 1 GGTFSCHFGPLTWCKPQGG 20

RESULT 40
US-09-052-889-34
; Sequence 34, Application US/09052889
; GENERAL INFORMATION:
; APPLICANT: Clark, Ross G.
; APPLICANT: Lowman, Henry B.
; APPLICANT: Robinson, Iain C.A.F.
; TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules
; NUMBER OF SEQUENCES: 79
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/052,889
; FILING DATE: 31-Mar-1998
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: P1071R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1896
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-052-889-34

Query Match 95.1%; Score 117; DB 14; Length 20;
Best Local Similarity 95.0%; Pred. No. 5e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
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Db 1 GGTYSCHFGPLTWCKPQGG 20
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RESULT 41
US-09-155-158-8
; Sequence 8, Application US/09155158
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; Dower, William J.
; Chang, Ray S.
; Kashyap, Arun K.
; Jolliffe, Linda K.
; Johnson, Dana
; Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; Erythropoietin Receptor
; NUMBER OF SEQUENCES: 262
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Affymax Research Institute
; STREET: 4001 Miranda Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,158
; FILING DATE: 03-Jun-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/09810
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: US 08/484,635
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/484,631
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Stracker, Elaine C.
; REGISTRATION NUMBER: 43,166
; REFERENCE/DOCKET NUMBER: 1053.3W
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 812-8700
; TELEFAX: (650) 424-0832
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-155-158-8
Query Match 95.1%; Score 117; DB 15; Length 20;
Best Local Similarity 95.0%; Pred. No. 5e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GGATSCHFGLTWCKPQGG 20
Db 1 GGTSCHFGLTWCKPQGG 20
RESULT 42
US-09-155-158-190
; Sequence 190, Application US/09155158
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; Dower, William J.
; Chang, Ray S.
; Kashyap, Arun K.

; Jolliffe, Linda K.
; Johnson, Dana
; Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; Erythropoietin Receptor
; NUMBER OF SEQUENCES: 262
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Affymax Research Institute
; STREET: 4001 Miranda Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,158
; FILING DATE: 03-Jun-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/09810
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: US 08/484,635
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/484,631
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Stracker, Elaine C.
; REGISTRATION NUMBER: 43,166
; REFERENCE/DOCKET NUMBER: 1053.3W
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 812-8700
; TELEFAX: (650) 424-0832
; INFORMATION FOR SEQ ID NO: 190:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 190:
US-09-155-158-190
Query Match 95.1%; Score 117; DB 15; Length 20;
Best Local Similarity 95.0%; Pred. No. 5e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GGATSCHFGLTWCKPQGG 20
Db 1 GGTSCHFGLTWCKPQGG 20
RESULT 43
US-09-189-745-1
; Sequence 1, Application US/09189745
; GENERAL INFORMATION:
; APPLICANT: Wilson, Ian A.
; APPLICANT: Livnah, Oded
; APPLICANT: Stura, Enrico A.
; APPLICANT: Johnson, Dana L.
; APPLICANT: Jolliffe, Linda K.
; TITLE OF INVENTION: SMALL MOLECULE MIMETICS OF
; ERYTHROPOIETIN
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston

; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/189,745
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/641,071
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07300/037001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-189-745-1

Query Match 95.1%; Score 117; DB 15; Length 20;
Best Local Similarity 95.0%; Pred. No. 5e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
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Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 44
US-09-341-590-117
; Sequence 117, Application US/09341590
; GENERAL INFORMATION:
; APPLICANT: Larsen, Bjarne Due
; TITLE OF INVENTION: PHARMACOLOGICALLY ACTIVE PEPTIDE CONJUGATES HAVING A
; TITLE OF INVENTION: REDUCED TENDENCY TOWARD ENZYMATIC HYDROLYSIS
; FILE REFERENCE: PPT-20479-US
; CURRENT APPLICATION NUMBER: US/09/341,590
; CURRENT FILING DATE: 1999-07-03
; PRIOR APPLICATION NUMBER: DK 0317/98
; PRIOR FILING DATE: 1998-03-09
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 117
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: EMP-1
; US-09-341-590-117

Query Match 95.1%; Score 117; DB 17; Length 20;
Best Local Similarity 95.0%; Pred. No. 5e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| ||||| |||||
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 45
US-09-428-082-87

; Sequence 87, Application US/09428082
; GENERAL INFORMATION:
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: FEIGE, ULRICH
; APPLICANT: CHEETHAM, JANET
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/09/428,082
; CURRENT FILING DATE: 1999-10-22
; EARLIER APPLICATION NUMBER: 60/105,371
; EARLIER FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 87
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: EPO-MIMETIC
; OTHER INFORMATION: PEPTIDE
; US-09-428-082-87

Query Match 95.1%; Score 117; DB 18; Length 20;
Best Local Similarity 95.0%; Pred. No. 5e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| ||||| |||||
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 46
US-09-428-082-1025
; Sequence 1025, Application US/09428082
; GENERAL INFORMATION:
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: FEIGE, ULRICH
; APPLICANT: CHEETHAM, JANET
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/09/428,082
; CURRENT FILING DATE: 1999-10-22
; EARLIER APPLICATION NUMBER: 60/105,371
; EARLIER FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1025
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: EPO MIMETIC
; OTHER INFORMATION: PEPTIDE
; US-09-428-082-1025

Query Match 95.1%; Score 117; DB 18; Length 20;
Best Local Similarity 95.0%; Pred. No. 5e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
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Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 47
US-09-428-082B-87
; Sequence 87, Application US/09428082B
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.

; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 87
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
US-09-428-082B-87

Query Match 95.1%; Score 117; DB 18; Length 20;
Best Local Similarity 95.0%; Pred. No. 5e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 48
US-09-428-082B-93
; Sequence 93, Application US/09428082B
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 93
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
; NAME/KEY: misc_feature
; LOCATION: (20)-(20)
; OTHER INFORMATION: Position 20, amino acid linker to an identical sequence
US-09-428-082B-93

Query Match 95.1%; Score 117; DB 18; Length 20;
Best Local Similarity 95.0%; Pred. No. 5e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 49
US-09-428-082B-1025
; Sequence 1025, Application US/09428082B
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527

; CURRENT APPLICATION NUMBER: US/09/428,082B
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1025
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
US-09-428-082B-1025

Query Match 95.1%; Score 117; DB 18; Length 20;
Best Local Similarity 95.0%; Pred. No. 5e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 50
US-09-563-286B-87
; Sequence 87, Application US/09563286B
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; APPLICANT: GUDAS, JEAN MARIE
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527A
; CURRENT APPLICATION NUMBER: US/09/563,286B
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/428,082
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1151
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 87
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-mimetic peptide
US-09-563-286B-87

Query Match 95.1%; Score 117; DB 19; Length 20;
Best Local Similarity 95.0%; Pred. No. 5e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTYSCHFGPLTWCKPQGG 20

Search completed: November 5, 2003, 19:10:55
Job time : 173 secs

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OM protein - protein search, using sw model

Run on: November 5, 2003, 19:05:59 ; Search time 18 Seconds
(without alignments)
52.234 Million cell updates/sec

Title: US-09-863-600E-19
Perfect score: 123
Sequence: 1 GGTASCHFGPLTWCKPQGG 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 248976 seqs, 47010500 residues

Total number of hits satisfying chosen parameters: 248976

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Pending Patents_AA_New:*
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2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep.*
3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep.*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep.*
5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep.*
6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep.*
7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	117	95.1	20	1	PCT-US03-18645-7
2	117	95.1	20	1	PCT-US03-26779-11
3	117	95.1	20	1	PCT-US03-26779-25
4	117	95.1	20	1	PCT-US03-26778-11
5	117	95.1	20	1	PCT-US03-26818-11
6	117	95.1	20	5	US-09-341-590A-117
7	117	95.1	20	6	US-10-651-723-87
8	117	95.1	20	6	US-10-651-723-93
9	117	95.1	20	6	US-10-651-723-1025
10	117	95.1	20	6	US-10-653-048-87
11	117	95.1	20	6	US-10-653-048-93
12	117	95.1	20	6	US-10-653-048-1025
13	117	95.1	20	6	US-10-666-696-87
14	117	95.1	20	6	US-10-666-696-93
15	117	95.1	20	6	US-10-666-696-1025
16	117	95.1	20	7	US-60-485-404-11
17	117	95.1	20	7	US-60-485-404-25
18	117	95.1	22	6	US-10-651-723-97
19	117	95.1	22	6	US-10-651-048-97
20	117	95.1	22	6	US-10-666-696-97
21	117	95.1	23	6	US-10-651-723-94
22	117	95.1	23	6	US-10-651-723-96
23	117	95.1	23	6	US-10-651-723-98
24	117	95.1	23	6	US-10-653-048-94
25	117	95.1	23	6	US-10-653-048-96
26	117	95.1	23	6	US-10-653-048-98
27	117	95.1	27	6	US-10-666-696-94
28	117	95.1	23	6	US-10-666-696-96
29	117	95.1	23	6	US-10-666-696-98
30	117	95.1	25	6	US-10-651-723-1034
31	117	95.1	25	6	US-10-653-048-1034
32	117	95.1	25	6	US-10-666-696-1034
33	117	95.1	36	6	US-10-651-723-403
34	117	95.1	36	6	US-10-653-048-403
35	117	95.1	36	6	US-10-666-696-403
36	117	95.1	39	6	US-10-651-723-395
37	117	95.1	39	6	US-10-653-048-395
38	117	95.1	39	6	US-10-666-696-395
39	117	95.1	40	6	US-10-651-723-92
40	117	95.1	40	6	US-10-653-048-92
41	117	95.1	40	6	US-10-666-696-92
42	117	95.1	46	6	US-10-651-723-95
43	117	95.1	46	6	US-10-653-048-95
44	117	95.1	46	6	US-10-666-696-95
45	117	95.1	49	6	US-10-651-723-339
46	117	95.1	49	6	US-10-651-723-340
47	117	95.1	49	6	US-10-653-048-339
48	117	95.1	49	6	US-10-666-696-339
49	117	95.1	49	6	US-10-666-696-340
50	117	95.1	51	6	US-10-651-723-417
51	117	95.1	57	6	US-10-653-048-417
52	117	95.1	57	6	US-10-666-696-417
53	117	95.1	253	6	US-10-651-723-16
54	117	95.1	253	6	US-10-651-723-18
55	117	95.1	253	6	US-10-653-048-16
56	117	95.1	253	6	US-10-653-048-18
57	117	95.1	253	6	US-10-666-696-16
58	117	95.1	253	6	US-10-666-696-18
59	117	95.1	277	6	US-10-651-723-20
60	117	95.1	277	6	US-10-651-723-22
61	117	95.1	277	6	US-10-653-048-20
62	117	95.1	277	6	US-10-653-048-22
63	117	95.1	277	6	US-10-666-696-20
64	117	95.1	277	6	US-10-666-696-22
65	117	95.1	18	6	US-10-651-723-425
66	105	85.4	18	6	US-10-651-723-1036
67	105	85.4	18	6	US-10-653-048-425
68	105	85.4	18	6	US-10-666-696-425
69	105	85.4	18	6	US-10-666-696-1036
70	105	85.4	18	6	US-10-666-696-422
71	105	85.4	19	6	US-10-651-723-422
72	100.5	81.7	19	6	US-10-653-048-422
73	100.5	81.7	19	6	US-10-666-696-422
74	100.5	81.7	26	5	US-09-341-590A-93
75	95	77.2	26	5	US-09-341-590A-94
76	95	77.2	32	5	US-09-341-590A-95
77	95	77.2	20	1	PCT-US03-18645-10
78	89	72.4	20	6	US-10-651-723-90
79	89	72.4	20	6	US-10-651-723-1029
80	89	72.4	20	6	US-10-653-048-90
81	89	72.4	20	6	US-10-666-696-90
82	89	72.4	20	6	US-10-666-696-1029
83	89	72.4	20	6	PCT-US03-18645-8
84	89	72.4	20	6	US-10-651-723-88
85	85	69.1	20	6	US-10-651-723-1026
86	85	69.1	20	6	US-10-653-048-88
87	85	69.1	20	6	US-10-653-048-1026
88	85	69.1	20	6	US-10-666-696-88
89	85	69.1	20	6	US-10-666-696-1026
90	85	69.1	20	1	PCT-US03-18645-9
91	85	69.1	20	6	US-10-651-723-89
92	81	65.9	20	6	US-10-651-723-426
93	81	65.9	20	6	US-10-651-723-1030
94	81	65.9	20	6	US-10-651-723-1037
95	81	65.9	20	6	US-10-653-048-89
96	81	65.9	20	6	US-10-653-048-426
97	81	65.9	20	6	US-10-653-048-1030
98	81	65.9	20	6	US-10-653-048-426
99	81	65.9	20	6	US-10-653-048-1030

100 81 65.9 20 6 US-10-653-048-1037 Sequence 1037, Ap

ALIGNMENTS

RESULT 1
PCT-US03-18645-7
; Sequence 7, Application PC/TUS0318645
; GENERAL INFORMATION:
; APPLICANT: The Burnham Institute
; APPLICANT: Digicaylioglu, Murat
; APPLICANT: Lipton, Stuart A.
; TITLE OF INVENTION: Neuroprotective Synergy of
; FILE REFERENCE: Erythropoietin and Insulin-Like Growth Factors
; CURRENT APPLICATION NUMBER: PCT/US03/18645
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: US 60/388,058
; PRIOR FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: US 60/458,145
; PRIOR FILING DATE: 2003-03-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
PCT-US03-18645-7

Query Match 95.1%; Score 117; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.6e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
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Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 2
PCT-US03-26779-11
; Sequence 11, Application PC/TUS0326779
; GENERAL INFORMATION:
; APPLICANT: Prior, Christopher P.
; APPLICANT: Turner, Andrew J.
; APPLICANT: Sadeghi, Homayoun
; TITLE OF INVENTION: Transferrin Fusion Protein Libraries
; FILE REFERENCE: 054710-5007-WO
; CURRENT APPLICATION NUMBER: PCT/US03/26779
; CURRENT FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: US 60/406,977
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 10/384,060
; PRIOR FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: US 60/485,404
; PRIOR FILING DATE: 2003-07-09
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: EPO mimetic
; OTHER INFORMATION: peptide
PCT-US03-26779-11

Query Match 95.1%; Score 117; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.6e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| ||||| |||||
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 3
PCT-US03-26779-25
; Sequence 25, Application PC/TUS0326779
; GENERAL INFORMATION:
; APPLICANT: Prior, Christopher P.
; APPLICANT: Turner, Andrew J.
; APPLICANT: Sadeghi, Homayoun
; TITLE OF INVENTION: Transferrin Fusion Protein Libraries
; FILE REFERENCE: 054710-5007-WO
; CURRENT APPLICATION NUMBER: PCT/US03/26779
; CURRENT FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: US 60/406,977
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 10/384,060
; PRIOR FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: US 60/485,404
; PRIOR FILING DATE: 2003-07-09
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: EPO mimetic
; OTHER INFORMATION: sequences
PCT-US03-26779-25

Query Match 95.1%; Score 117; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.6e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| ||||| |||||
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 4
PCT-US03-26778-11
; Sequence 11, Application PC/TUS0326778
; GENERAL INFORMATION:
; APPLICANT: Prior, Christopher P.
; APPLICANT: Sadeghi, Homayoun
; APPLICANT: Turner, Andrew J.
; TITLE OF INVENTION: ORAL DELIVERY OF MODIFIED TRANSFERRIN FUSION PROTEINS
; FILE REFERENCE: 54710-5006-WO
; CURRENT APPLICATION NUMBER: PCT/US03/26778
; CURRENT FILING DATE: 2003-08-28
; PRIOR APPLICATION NUMBER: US 60/406,977
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 10/378,094
; PRIOR FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: US 60/460,829
; PRIOR FILING DATE: 2003-04-08
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: EMP1 peptide
PCT-US03-26778-11

Query Match 95.1%; Score 117; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.6e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| ||||| ||||| |||||
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 5

PCT-US03-26818-11
; Sequence 11, Application PC/TUS0326818
; GENERAL INFORMATION:
; APPLICANT: PRIOR, Christopher P.
; APPLICANT: LAI, Char-Huei
; APPLICANT: SADEGHI, Homayoun
; APPLICANT: TURNER, Andrew J.
; TITLE OF INVENTION: MODIFIED TRANSFERRIN FUSION PROTEINS
; FILE REFERENCE: 54710-5001-01-WO
; CURRENT APPLICATION NUMBER: PCT/US03/26818
; CURRENT FILING DATE: 2003-08-28
; PRIOR APPLICATION NUMBER: US 60/406,977
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 10/378,094
; PRIOR FILING DATE: 2003-03-04
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: EMP1 peptide
PCT-US03-26818-11

Query Match 95.1%; Score 117; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.6e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| ||||| ||||| |||||
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 6

US-09-341-590A-117
; Sequence 117, Application US/09341590A
; GENERAL INFORMATION:
; APPLICANT: LARSEN, BJARNE DUE
; TITLE OF INVENTION: PHARMACOLOGICALLY ACTIVE PEPTIDE CONJUGATES HAVING A
; TITLE OF INVENTION: REDUCED TENDENCY TOWARDS ENZYMATIC HYDROLYSIS
; FILE REFERENCE: 55508(45487)
; CURRENT APPLICATION NUMBER: US/09/341,590A
; CURRENT FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: DK 0317/98
; PRIOR FILING DATE: 1998-03-09
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 117
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: EMP-1
US-09-341-590A-117

Query Match 95.1%; Score 117; DB 5; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.6e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| ||||| ||||| |||||
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 7

US-10-651-723-87

; Sequence 87, Application US/10651723
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/651,723
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 87
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
US-10-651-723-87

Query Match 95.1%; Score 117; DB 6; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.6e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| ||||| ||||| |||||
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 8

US-10-651-723-93
; Sequence 93, Application US/10651723
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/651,723
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 93
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
; NAME/KEY: misc_feature
; LOCATION: (20)..(20)
; OTHER INFORMATION: Position 20, amino acid linker to an identical sequence
US-10-651-723-93

Query Match 95.1%; Score 117; DB 6; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.6e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| ||||| ||||| |||||
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 9

US-10-651-723-1025
; Sequence 1025, Application US/10651723
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/651,723
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1025
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
; NAME/KEY: misc.feature
; LOCATION: (20)..(20)
; OTHER INFORMATION: Position 20, amino acid linker to an identical sequence
US-10-651-723-1025

Query Match 95.1%; Score 117; DB 6; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.6e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| ||||| |||||
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 10
US-10-653-048-87
; Sequence 87, Application US/10653048
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/653,048
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 87
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
US-10-653-048-87

Query Match 95.1%; Score 117; DB 6; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.6e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| ||||| |||||
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 11
US-10-653-048-93
; Sequence 93, Application US/10653048
; GENERAL INFORMATION:

; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/653,048
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 93
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
; NAME/KEY: misc.feature
; LOCATION: (20)..(20)
; OTHER INFORMATION: Position 20, amino acid linker to an identical sequence
US-10-653-048-93

Query Match 95.1%; Score 117; DB 6; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.6e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| ||||| |||||
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 12
US-10-653-048-1025
; Sequence 1025, Application US/10653048
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/653,048
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1025
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
US-10-653-048-1025

Query Match 95.1%; Score 117; DB 6; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.6e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| ||||| |||||
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 13
US-10-666-696-87
; Sequence 87, Application US/10666696

GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; APPLICANT: GUDAS, JEAN MARIE
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527A
; CURRENT APPLICATION NUMBER: US/10/666,696
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/563,286C
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/428,082
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1157
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 87
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-mimetic peptide
US-10-666-696-87

Query Match 95.1%; Score 117; DB 6; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.6e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTYSCHFGLTWCKPQGG 20

RESULT 14
US-10-666-696-93
; Sequence 93, Application US/10666696
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; APPLICANT: GUDAS, JEAN MARIE
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527A
; CURRENT APPLICATION NUMBER: US/10/666,696
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/563,286C
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/428,082
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1157
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 93
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-mimetic peptide
; NAME/KEY: misc_feature
; LOCATION: (20)..(20)
; OTHER INFORMATION: Position 20, amino acid linker to an identical sequence
US-10-666-696-93

Query Match 95.1%; Score 117; DB 6; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.6e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20

Db 1 GGTYSCHFGLTWCKPQGG 20
RESULT 15
US-10-666-696-1025
; Sequence 1025, Application US/10666696
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; APPLICANT: GUDAS, JEAN MARIE
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527A
; CURRENT APPLICATION NUMBER: US/10/666,696
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/563,286C
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/428,082
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1157
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1025
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
US-10-666-696-1025

Query Match 95.1%; Score 117; DB 6; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.6e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTYSCHFGLTWCKPQGG 20

RESULT 16
US-60-485-404-11
; Sequence 11, Application US/60485404
; GENERAL INFORMATION:
; APPLICANT: Prior, Christopher P.
; APPLICANT: Turner, Andrew J.
; APPLICANT: Sadeghi, Homayoun
; TITLE OF INVENTION: Transferrin Fusion Protein Libraries
; FILE REFERENCE: 054710-5007-PR
; CURRENT APPLICATION NUMBER: US/60/485,404
; CURRENT FILING DATE: 2003-07-09
; PRIOR APPLICATION NUMBER: US 10/231,494
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/406,997
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 10/384,060
; PRIOR FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: US 60/460,829
; PRIOR FILING DATE: 2003-04-08
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: EPO mimetic
; OTHER INFORMATION: peptide
US-60-485-404-11

Query Match 95.1%; Score 117; DB 7; Length 20;

```
; Rest Local Similarity 95.0%; Pred. No. 1.6e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
   ||| ||||| ||||| |||||
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 17
US-60-485-404-25
; Sequence 25, Application US/60485404
; GENERAL INFORMATION:
; APPLICANT: Prior, Christopher P.
; APPLICANT: Turner, Andrew J.
; APPLICANT: Sadeghi, Homayoun
; TITLE OF INVENTION: Transferrin Fusion Protein Libraries
; FILE REFERENCE: 054710-5007-PR
; CURRENT APPLICATION NUMBER: US/60/485,404
; CURRENT FILING DATE: 2003-07-09
; PRIOR APPLICATION NUMBER: US 10/231,494
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/406,997
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 10/384,060
; PRIOR FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: US 60/460,829
; PRIOR FILING DATE: 2003-04-08
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 25
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: EPO mimetic
; OTHER INFORMATION: sequences
US-60-485-404-25

Query Match 95.1%; Score 117; DB 7; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.6e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
   ||| ||||| ||||| |||||
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 18
US-10-651-723-97
; Sequence 97, Application US/10651723
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/651,723
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 97
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (22)..(22)
; OTHER INFORMATION: Position 22 linked through epsilon amine to lysyl, which is li
; OTHER INFORMATION: d to a separate identical sequence through that sequence's alp
; OTHER INFORMATION: amine
US-10-651-723-97

Query Match 95.1%; Score 117; DB 6; Length 22;
Best Local Similarity 95.0%; Pred. No. 1.7e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
   ||| ||||| ||||| |||||
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 20
US-10-666-696-97
; Sequence 97, Application US/10666696
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; APPLICANT: GUDAS, JEAN MARIE
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527A
; CURRENT APPLICATION NUMBER: US/10/666,696
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/563,286C
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/428,082
; PRIOR FILING DATE: 1999-10-22
```

; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1157
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 97
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (22)..(22)
; OTHER INFORMATION: Position 22 linked through epsilon amine to lysyl, which is linked
; OTHER INFORMATION: d to a separate identical sequence through that sequence's alpha
; OTHER INFORMATION: amine
US-10-666-696-97

Query Match 95.1%; Score 117; DB 6; Length 22;
Best Local Similarity 95.0%; Pred. No. 1.7e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| ||||| |||||
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 21

US-10-651-723-94
; Sequence 94, Application US/10651723
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/651,723
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 94
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
US-10-651-723-94

Query Match 95.1%; Score 117; DB 6; Length 23;
Best Local Similarity 95.0%; Pred. No. 1.8e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| ||||| |||||
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 22

US-10-651-723-96
; Sequence 96, Application US/10651723
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/651,723

; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 96
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (23)..(23)
; OTHER INFORMATION: Position 23, amino acid linker to an identical sequence
US-10-651-723-96

Query Match 95.1%; Score 117; DB 6; Length 23;
Best Local Similarity 95.0%; Pred. No. 1.8e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| ||||| |||||
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 23

US-10-651-723-98
; Sequence 98, Application US/10651723
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/651,723
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 98
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (23)..(23)
; OTHER INFORMATION: At position 23 biotin linked to the sidechain through a linker
US-10-651-723-98

Query Match 95.1%; Score 117; DB 6; Length 23;
Best Local Similarity 95.0%; Pred. No. 1.8e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| ||||| |||||
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 24

US-10-653-048-94
; Sequence 94, Application US/10653048
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA


```

; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/653,048
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 94
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
US-10-653-048-94

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Query Match          95.1%; Score 117; DB 6; Length 23;
Best Local Similarity 95.0%; Pred. No. 1.8e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTYSCHFGPLTWCKPQGG 20

```

RESULT 25

US-10-653-048-96

; Sequence 96, Application US/10653048

; GENERAL INFORMATION:

; APPLICANT: FEIGE, ULRICH

; APPLICANT: LIU, CHUAN-FA

; APPLICANT: CHEETHAM, JANET C.

; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS

; FILE REFERENCE: A-527

; CURRENT APPLICATION NUMBER: US/10/653,048

; CURRENT FILING DATE: 2003-08-29

; PRIOR APPLICATION NUMBER: US/09/428,082B

; PRIOR FILING DATE: 1999-10-22

; PRIOR APPLICATION NUMBER: 60/105,371

; PRIOR FILING DATE: 1998-10-23

; NUMBER OF SEQ ID NOS: 1133

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 96

; LENGTH: 23

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (23)..(23)

; OTHER INFORMATION: Position 23, amino acid linker to an identical sequence

US-10-653-048-96

```

Query Match          95.1%; Score 117; DB 6; Length 23;
Best Local Similarity 95.0%; Pred. No. 1.8e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTYSCHFGPLTWCKPQGG 20

```

RESULT 26

US-10-653-048-98

; Sequence 98, Application US/10653048

; GENERAL INFORMATION:

; APPLICANT: FEIGE, ULRICH

```

; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/653,048
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 98
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (23)..(23)
; OTHER INFORMATION: At position 23 biotin linked to the sidechain through a linker
US-10-653-048-98

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```

Query Match          95.1%; Score 117; DB 6; Length 23;
Best Local Similarity 95.0%; Pred. No. 1.8e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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```

QY 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTYSCHFGPLTWCKPQGG 20

```

RESULT 27

US-10-666-696-94

; Sequence 94, Application US/10666696

; GENERAL INFORMATION:

; APPLICANT: FEIGE, ULRICH

; APPLICANT: LIU, CHUAN-FA

; APPLICANT: CHEETHAM, JANET C.

; APPLICANT: BOONE, THOMAS CHARLES

; APPLICANT: GUDAS, JEAN MARIE

; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS

; FILE REFERENCE: A-527A

; CURRENT APPLICATION NUMBER: US/10/666,696

; CURRENT FILING DATE: 2003-09-19

; PRIOR APPLICATION NUMBER: US/09/563,286C

; PRIOR FILING DATE: 2000-05-03

; PRIOR APPLICATION NUMBER: 09/428,082

; PRIOR FILING DATE: 1999-10-22

; PRIOR APPLICATION NUMBER: 60/105,371

; PRIOR FILING DATE: 1998-10-23

; NUMBER OF SEQ ID NOS: 1157

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 94

; LENGTH: 23

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: EPO-mimetic peptide

US-10-666-696-94

```

Query Match          95.1%; Score 117; DB 6; Length 23;
Best Local Similarity 95.0%; Pred. No. 1.8e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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```

QY 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTYSCHFGPLTWCKPQGG 20

```

RESULT 28

US-10-666-696-96
; Sequence 96, Application US/10666696
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; APPLICANT: GUDAS, JEAN MARIE
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527A
; CURRENT APPLICATION NUMBER: US/10/666,696
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/563,286C
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/428,082
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1157
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 96
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-mimetic peptide
; NAME/KEY: misc_feature
; LOCATION: (23)..(23)
; OTHER INFORMATION: Position 23, amino acid linker to an identical sequence
US-10-666-696-96

Query Match 95.1%; Score 117; DB 6; Length 23;
Best Local Similarity 95.0%; Pred. No. 1.8e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
DB 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 29
US-10-666-696-98
; Sequence 98, Application US/10666696
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; APPLICANT: GUDAS, JEAN MARIE
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527A
; CURRENT APPLICATION NUMBER: US/10/666,696
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/563,286C
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/428,082
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1157
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 98
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-mimetic peptide
; NAME/KEY: misc_feature
; LOCATION: (23)..(23)
; OTHER INFORMATION: At position 23 biotin linked to the sidechain through a linker
US-10-666-696-98

Query Match 95.1%; Score 117; DB 6; Length 23;
Best Local Similarity 95.0%; Pred. No. 1.8e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
DB 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 30
US-10-651-723-1034
; Sequence 1034, Application US/10651723
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/651,723
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1034
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC
; NAME/KEY: misc_feature
; LOCATION: (25)..(25)
; OTHER INFORMATION: Fc domain attached at Position 25 of the C-terminus
US-10-651-723-1034

Query Match 95.1%; Score 117; DB 6; Length 25;
Best Local Similarity 95.0%; Pred. No. 1.9e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
DB 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 31
US-10-653-048-1034
; Sequence 1034, Application US/10653048
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/653,048
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1034
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC

```
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (25)..(25)
; OTHER INFORMATION: Fc domain attached at Position 25 of the C-terminus
US-10-653-048-1034

Query Match          95.1%; Score 117; DB 6; Length 25;
Best Local Similarity 95.0%; Pred. No. 1.9e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
   ||| ||||| ||||| |||||
Db 1 GGTYSCHFGLTWCKPQGG 20

RESULT 32
US-10-666-696-1034
; Sequence 1034, Application US/10666696
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; APPLICANT: GUDAS, JEAN MARIE
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527A
; CURRENT APPLICATION NUMBER: US/10/666,696
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/563,286C
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/428,082
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1157
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1034
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: TPO-MIMETIC
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Fc domain attached at Position 25 of the C-terminus
US-10-666-696-1034

Query Match          95.1%; Score 117; DB 6; Length 25;
Best Local Similarity 95.0%; Pred. No. 1.9e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
   ||| ||||| ||||| |||||
Db 1 GGTYSCHFGLTWCKPQGG 20

RESULT 33
US-10-651-723-403
; Sequence 403, Application US/10651723
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/651,723
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
```

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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 403
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EMP-Fc
US-10-651-723-403

Query Match          95.1%; Score 117; DB 6; Length 36;
Best Local Similarity 95.0%; Pred. No. 2.6e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
   ||| ||||| ||||| |||||
Db 12 GGTYSCHFGLTWCKPQGG 31

RESULT 34
US-10-653-048-403
; Sequence 403, Application US/10653048
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/653,048
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 403
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EMP-Fc
US-10-653-048-403

Query Match          95.1%; Score 117; DB 6; Length 36;
Best Local Similarity 95.0%; Pred. No. 2.6e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
   ||| ||||| ||||| |||||
Db 12 GGTYSCHFGLTWCKPQGG 31

RESULT 35
US-10-666-696-403
; Sequence 403, Application US/10666696
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; APPLICANT: GUDAS, JEAN MARIE
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527A
; CURRENT APPLICATION NUMBER: US/10/666,696
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/563,286C
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/428,082
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1157
```

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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 403
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EMP CONSTRUCT
US-10-666-696-403
```

```
Query Match          95.1%; Score 117; DB 6; Length 36;
Best Local Similarity 95.0%; Pred. No. 2.6e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 GGTASCHFGPLTWCKPQGG 20
      ||| ||||| ||||| |||||
DB      12 GGTYSCHFGPLTWCKPQGG 31
```

```
RESULT 36
US-10-651-723-395
; Sequence 395, Application US/10651723
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/651,723
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 395
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: FC-EMP
US-10-651-723-395
```

```
Query Match          95.1%; Score 117; DB 6; Length 39;
Best Local Similarity 95.0%; Pred. No. 2.8e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 GGTASCHFGPLTWCKPQGG 20
      ||| ||||| ||||| |||||
DB      8 GGTYSCHFGPLTWCKPQGG 27
```

```
RESULT 37
US-10-653-048-395
; Sequence 395, Application US/10653048
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/653,048
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 395
; LENGTH: 39
```

```
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: FC-EMP
US-10-653-048-395
```

```
Query Match          95.1%; Score 117; DB 6; Length 39;
Best Local Similarity 95.0%; Pred. No. 2.8e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 GGTASCHFGPLTWCKPQGG 20
      ||| ||||| ||||| |||||
DB      8 GGTYSCHFGPLTWCKPQGG 27
```

```
RESULT 38
US-10-666-696-395
; Sequence 395, Application US/10666696
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; APPLICANT: GUDAS, JEAN MARIE
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527A
; CURRENT APPLICATION NUMBER: US/10/666,696
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/563,286C
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/428,082
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1157
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 395
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SEQUENCE COMPRISING PL PROMOTER USED TO CONSTRUCT EMP
US-10-666-696-395
```

```
Query Match          95.1%; Score 117; DB 6; Length 39;
Best Local Similarity 95.0%; Pred. No. 2.8e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 GGTASCHFGPLTWCKPQGG 20
      ||| ||||| ||||| |||||
DB      8 GGTYSCHFGPLTWCKPQGG 27
```

```
RESULT 39
US-10-651-723-92
; Sequence 92, Application US/10651723
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/651,723
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 92
; LENGTH: 40
```

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
US-10-651-723-92

Query Match 95.1%; Score 117; DB 6; Length 40;
Best Local Similarity 95.0%; Pred. No. 2.8e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| ||||| |||||
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 40
US-10-653-048-92
; Sequence 92, Application US/10653048
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/653,048
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 92
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
US-10-653-048-92

Query Match 95.1%; Score 117; DB 6; Length 40;
Best Local Similarity 95.0%; Pred. No. 2.8e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| ||||| |||||
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 41
US-10-666-696-92
; Sequence 92, Application US/10666696
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; APPLICANT: GUDAS, JEAN MARIE
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527A
; CURRENT APPLICATION NUMBER: US/10/666,696
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/563,286C
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/428,082
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1157
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 92
; LENGTH: 40

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-mimetic peptide
US-10-666-696-92

Query Match 95.1%; Score 117; DB 6; Length 40;
Best Local Similarity 95.0%; Pred. No. 2.8e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| ||||| |||||
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 42
US-10-651-723-95
; Sequence 95, Application US/10651723
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/651,723
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 95
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
US-10-651-723-95

Query Match 95.1%; Score 117; DB 6; Length 46;
Best Local Similarity 95.0%; Pred. No. 3.2e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| ||||| |||||
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 43
US-10-653-048-95
; Sequence 95, Application US/10653048
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/653,048
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 95
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

```
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
US-10-653-048-95

Query Match          95.1%; Score 117; DB 6; Length 46;
Best Local Similarity 95.0%; Pred. No. 3.2e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 44
US-10-666-696-95
; Sequence 95, Application US/10666696
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; APPLICANT: GUDAS, JEAN MARIE
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527A
; CURRENT APPLICATION NUMBER: US/10/666,696
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/563,286C
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/428,082
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1157
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 95
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-mimetic peptide
US-10-666-696-95

Query Match          95.1%; Score 117; DB 6; Length 46;
Best Local Similarity 95.0%; Pred. No. 3.2e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 45
US-10-651-723-339
; Sequence 339, Application US/10651723
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/651,723
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 339
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
```

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; OTHER INFORMATION: EPO-MIMETIC
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: Fc domain attached at Position 1 of the N-terminus
US-10-651-723-339

Query Match          95.1%; Score 117; DB 6; Length 49;
Best Local Similarity 95.0%; Pred. No. 3.4e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
Db 6 GGTYSCHFGPLTWCKPQGG 25

RESULT 46
US-10-651-723-340
; Sequence 340, Application US/10651723
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/651,723
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 340
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (49)..(49)
; OTHER INFORMATION: Fc domain attached at Position 49 of the C-terminus
US-10-651-723-340

Query Match          95.1%; Score 117; DB 6; Length 49;
Best Local Similarity 95.0%; Pred. No. 3.4e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 47
US-10-653-048-339
; Sequence 339, Application US/10653048
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/653,048
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; FEATURE:
```

```
; SEQ ID NO 339
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC
; NAME/KEY: misc feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: Fc domain attached at Position 1 of the N-terminus
US-10-653-048-339

Query Match          95.1%; Score 117; DB 6; Length 49;
Best Local Similarity 95.0%; Pred. No. 3.4e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
   ||| ||||| ||||| ||||| |||||
Db 6 GGTYSCHFGPLTWCKPQGG 25

RESULT 48
US-10-653-048-340
; Sequence 340, Application US/10653048
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/653,048
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 340
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC
; NAME/KEY: misc feature
; LOCATION: (49)..(49)
; OTHER INFORMATION: Fc domain attached at Position 49 of the C-terminus
US-10-653-048-340

Query Match          95.1%; Score 117; DB 6; Length 49;
Best Local Similarity 95.0%; Pred. No. 3.4e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
   ||| ||||| ||||| ||||| |||||
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 49
US-10-666-696-339
; Sequence 339, Application US/10666696
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; APPLICANT: GUDAS, JEAN MARIE
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527A
; CURRENT APPLICATION NUMBER: US/10/666,696
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/563,286C
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/428,082
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1157
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 340
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC
; NAME/KEY: misc feature
; OTHER INFORMATION: Fc domain attached at Position 49 of the C-terminus
US-10-666-696-340

Query Match          95.1%; Score 117; DB 6; Length 49;
Best Local Similarity 95.0%; Pred. No. 3.4e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
   ||| ||||| ||||| ||||| |||||
Db 1 GGTYSCHFGPLTWCKPQGG 20

Search completed: November 5, 2003, 19:11:24
Job time : 18 secs
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; PRIOR APPLICATION NUMBER: US/09/563,286C
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/428,082
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1157
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 339
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC
; NAME/KEY: misc feature
; OTHER INFORMATION: Fc domain attached at Position 1 of the N-terminus
US-10-666-696-339
```

```
Query Match          95.1%; Score 117; DB 6; Length 49;
Best Local Similarity 95.0%; Pred. No. 3.4e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 GGTASCHFGPLTWCKPQGG 20
   ||| ||||| ||||| ||||| |||||
Db 6 GGTYSCHFGPLTWCKPQGG 25
```

```
RESULT 50
US-10-666-696-340
; Sequence 340, Application US/10666696
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; APPLICANT: GUDAS, JEAN MARIE
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527A
; CURRENT APPLICATION NUMBER: US/10/666,696
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/563,286C
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/428,082
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1157
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 340
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC
; NAME/KEY: misc feature
; OTHER INFORMATION: Fc domain attached at Position 49 of the C-terminus
US-10-666-696-340
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Query Match          95.1%; Score 117; DB 6; Length 49;
Best Local Similarity 95.0%; Pred. No. 3.4e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1 GGTASCHFGPLTWCKPQGG 20
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Db 1 GGTYSCHFGPLTWCKPQGG 20
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Search completed: November 5, 2003, 19:11:24
Job time : 18 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 5, 2003, 18:59:48 ; Search time 41 Seconds
(without alignments)
77.428 Million cell updates/sec

Title: US-09-863-600E-19
Perfect score: 123
Sequence: 1 GGTASCHFGPLTWVCKPQG 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	123	100.0	20	AA13641	Erythropoietin rec
2	123	100.0	20	AAU74467	Human erythropoiet
3	119	96.7	20	AA13645	Erythropoietin rec
4	119	96.7	20	AAU74477	Human erythropoiet
5	119	96.7	20	AAU74485	Human erythropoiet
6	117	95.1	20	AAU26550	Erythropoietin rec
7	117	95.1	20	AAU26481	Erythropoietin rec
8	117	95.1	20	AAU26406	Erythropoietin rec
9	117	95.1	20	AAU26387	Erythropoietin rec

10	117	95.1	20	18	AAV26399	Erythropoietin rec
11	117	95.1	20	18	AAV26372	Erythropoietin rec
12	117	95.1	20	18	AAV13646	Erythropoietin rec
13	117	95.1	20	18	AAV13683	Erythropoietin rec
14	117	95.1	20	18	AAW43020	Peptide mimetic of
15	117	95.1	20	18	AAW26963	Monomer subunit of
16	117	95.1	20	18	AAW26975	Monomer subunit of
17	117	95.1	20	18	AAW26997	Monomer subunit of
18	117	95.1	20	21	AA13501	Erythropoietin der
19	117	95.1	20	21	AA17031	EPO-mimetic peptid
20	117	95.1	20	21	AA17921	EPO-mimetic peptid
21	117	95.1	20	22	AG63738	Peptide agonist fo
22	117	95.1	20	22	AA897489	Erythropoietin cyc
23	117	95.1	20	22	AA897492	Erythropoietin cyc
24	117	95.1	20	23	AAU74456	Human erythropoiet
25	117	95.1	20	23	AAU74478	Human erythropoiet
26	117	95.1	20	23	AAU74486	Human erythropoiet
27	117	95.1	20	23	ABB72814	Erythropoietin (EP
28	117	95.1	20	23	ABB72840	Erythropoietin (EP
29	117	95.1	20	23	ABB57650	Erythropoietin rec
30	117	95.1	22	18	AA13638	Erythropoietin rec
31	117	95.1	22	21	AA17041	EPO-mimetic peptid
32	117	95.1	22	23	ABB72824	Erythropoietin (EP
33	117	95.1	23	18	AAV26551	Erythropoietin rec
34	117	95.1	23	21	AA17038	EPO-mimetic peptid
35	117	95.1	23	21	AA17042	EPO-mimetic peptid
36	117	95.1	23	23	ABB72821	Erythropoietin (EP
37	117	95.1	24	23	ABB72825	Erythropoietin (EP
38	117	95.1	25	23	ABB73394	EPO-mimetic peptid
39	117	95.1	26	21	AA17930	EPO-mimetic peptid
40	117	95.1	36	21	AA17313	EMP-Fc fusion cons
41	117	95.1	36	23	ABB73407	EPO mimetic peptid
42	117	95.1	39	21	AA17312	Fc-EMP fusion cons
43	117	95.1	39	23	ABB73406	EPO mimetic peptid
44	117	95.1	40	21	AA17036	EPO-mimetic peptid
45	117	95.1	40	23	ABB72819	Erythropoietin (EP
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47	117	95.1	41	23	ABB72820	Erythropoietin (EP
48	117	95.1	42	20	AAV49902	Erythropoietin rec
49	117	95.1	46	21	AA17039	EPO-mimetic peptid
50	117	95.1	46	23	ABB72822	Erythropoietin (EP
51	117	95.1	47	21	AA17040	EPO-mimetic peptid
52	117	95.1	47	23	ABB72823	Erythropoietin (EP
53	117	95.1	49	23	ABB73392	EPO-mimetic peptid
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56	117	95.1	50	21	AA17284	EPO-mimetic peptid
57	117	95.1	57	21	AA17314	EMP-EMP-Fc fusion
58	117	95.1	57	23	ABB73408	EMP-EMP gene const
59	117	95.1	253	21	AA16964	Fc-EMP protein seq
60	117	95.1	253	21	AA16965	EMP-Fc protein seq
61	117	95.1	253	23	ABB73415	Fc-EPO mimetic pep
62	117	95.1	253	23	ABB73416	EPO mimetic peptid
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64	117	95.1	277	21	AA16967	Fc-EMP-EMP protein
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66	117	95.1	278	23	ABB73417	EMP-EMP-Fc amino a
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68	112	91.1	20	18	AAV13650	Erythropoietin rec
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70	112	91.1	20	23	AAU74481	Human erythropoiet
71	111	90.2	20	18	AAV13625	Erythropoietin rec
72	111	90.2	20	18	AAV13649	Erythropoietin rec
73	111	90.2	20	23	AAU74468	Human erythropoiet
74	109	88.6	20	18	AAV13647	Erythropoietin rec
75	109	88.6	20	23	AAU74479	Human erythropoiet
76	109	88.6	20	23	AAU74484	Human erythropoiet
77	108.5	88.2	22	22	AA897497	Erythropoietin cyc
78	107	87.0	20	18	AAV13652	Erythropoietin rec
79	107	87.0	20	18	AAV13659	Erythropoietin rec
80	107	87.0	20	23	AAU74483	Human erythropoiet
81	105	85.4	18	18	AAV13626	Erythropoietin rec
82	105	85.4	18	18	AAV13633	Erythropoietin rec

83 105 85.4 18 18 AAY13657 Erythropoietin rec
84 105 85.4 18 18 AAW26968 Monomer subunit of
85 105 85.4 18 21 AAB13506 Erythropoietin der
86 105 85.4 18 21 AAB17321 EPO-mimetic peptid
87 105 85.4 18 21 AAB17932 EPO-mimetic peptid
88 105 85.4 18 22 AAB97494 Erythropoietin cyc
89 105 85.4 18 23 AAU74461 Human erythropoiet
90 105 85.4 18 23 AAU74470 Human erythropoiet
91 105 85.4 18 23 ABB72830 Erythropoietin (EP
92 105 85.4 18 23 ABB72845 Erythropoietin (EP
93 103 83.7 20 18 AAY13651 Erythropoietin rec
94 103 83.7 20 23 AAU74482 Human erythropoiet
95 102 82.9 20 22 AAU05325 R1 and R2 peptide
96 101 82.1 20 22 AAU05326 R1 and R2 peptide
97 100.5 81.7 19 21 AAB17318 EPO-mimetic peptid
98 100.5 81.7 19 23 ABB72827 Erythropoietin (EP
99 99 80.5 20 22 AAU05307 R1 and R2 peptide
100 99 80.5 20 22 AAU05315 R1 and R2 peptide

ALIGNMENTS

RESULT 1
ID AAY13641 standard; peptide; 20 AA.
XX
AC AAY13641;
XX
DT 06-SEP-1999 (first entry)
XX
DE Erythropoietin receptor (EPO-R) binding peptide.
XX
KW Erythropoietin; EPO; receptor; EPO deficiency; renal failure; AIDS;
KW dialysis; anaemia; autoimmune disease; chronic inflammatory disease;
KW malignancy; beta-thalassaemia; cystic fibrosis; prematurity; blood loss;
KW spinal cord injury; aging; neoplastic disease; erythropoiesis; EPO-R.
XX
OS Synthetic.
XX
PN WO9640749-A1.
XX
PD 19-DEC-1996.
XX
PF 07-JUN-1996; 96WO-US09810.
XX
PR 07-JUN-1995; 95US-0484635.
PR 07-JUN-1995; 95US-0484631.
PR 19-NOV-1993; 93US-0155940.
XX
(AFFY-) AFFYMAX TECHNOLOGIES NV.
PA (JOHJ) JOHNSON & JOHNSON CORP.
PA (ORTH) ORTHO PHARM CORP.
XX

Chang RS, Dower WJ, Johnson D, Jolliffe LK, Kashyap AK;
Mulcahy L, Wrighton NC;
WPI; 1997-052225/05.
XX
PT Erythropoietin receptor binding peptide - useful for treating
PT disorders characterised by deficiency of EPO, or low or defective
PT red blood cell population
XX
PS Claim 6; Page 68; 95pp; English.
XX
CC The invention describes a peptide of 10-40 amino acid residues which
CC binds to erythropoietin (EPO) receptor and which includes the amino acid
CC sequence Cys-Xaa1-Xaa2-Gly-Pro-Xaa3-Thr-Trp-Xaa4-Cys, where Xaa1 = Arg,
CC His, Leu or Trp, Xaa2 = Met, Phe or Ile, Xaa3 = 1 of the 20 genetically
CC coded L-amino acids, and Xaa4 = Asp, Glu, Ile, Leu or Val. Optionally,
CC the peptide may be cyclised or dimerised. The peptide can be used to
CC treat a patient having a disorder characterised by a deficiency of EPO
CC or a low or defective red blood cell population. It can be used to treat

CC end stage renal failure or dialysis; anaemia associated with AIDS,
CC autoimmune disease, chronic inflammatory diseases or malignancy;
CC beta-thalassaemia; cystic fibrosis; early anaemia of prematurity; spinal
CC cord injury; acute blood loss; aging; and neoplastic disease states
CC accompanied by abnormal erythropoiesis. The peptides can also be used as
CC reagents for detecting EPO receptors on living cells, in biological
CC fluids, in tissue homogenates, etc. Sequences AAY13624-661 represent
CC specific examples of EPO-R binding peptides.
XX
SQ Sequence 20 AA;
Query Match 100.0%; Score 123; DB 18; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTASCHFGPLTWCKPQGG 20

RESULT 2
ID AAU74467 standard; Peptide; 20 AA.
XX
AC AAU74467;
XX
DT 09-APR-2002 (first entry)
XX
DE Human erythropoietin neuroprotective peptide EMP-6.
XX
KW Neuroprotective peptide; human; erythropoietin; neurotoxicity; anaemia;
KW erythropoietin receptor; EPO receptor; neurodegeneration; prion disease;
KW neurological damage; neurodegenerative disorder; neurological disorder;
KW psychiatric disorder; blood loss; renal failure; cancer; HIV; EMP-6;
KW human immunodeficiency virus; haematology; autoimmune disease;
KW inflammatory disorder; infectious disease.
XX
OS Homo sapiens.
XX
PN WO200191780-A1.
XX
PD 06-DEC-2001.
XX
PF 23-MAY-2001; 2001WO-US16654.
XX
PR 26-MAY-2000; 2000US-207654P.
XX
PA (ORTH) ORTHO-MCNEIL PHARM INC.
XX
PI Smith-Swintosky V, Renzi M, Plata-Salaman C, Jolliffe L, Farrell F;
PI Johnson DL;
XX
DR WPI; 2002-114307/15.
XX
PT Treating patients having condition mediated by neurotoxicity,
PT neurodegeneration or neurological damage, involves administering to
PT patient a peptide comprising monomeric peptides that bind to
PT erythropoietin receptor -
XX
PS Claim 14; Page 40; 75pp; English.
XX
CC The invention relates to a method for treating a patient with a condition
CC mediated by neurotoxicity, neurodegeneration or neurological damage,
CC involving administering a peptide comprising one or more monomeric
CC peptides that bind to the human erythropoietin (EPO) receptor. The method
CC is useful for treating acute and chronic neurodegenerative disorders
CC including cerebral ischaemia or infarction, Alzheimer's disease, Pick's
CC disease, diffuse Lewy body disease, Shy-Drager syndrome, amyotrophic
CC lateral sclerosis, Huntington's disease, Parkinson's disease, Gilles De
CC La Tourette's disease, Tay-Sachs's disease, and prion diseases including
CC Creutzfeldt-Jakob and Kuru, neurological and psychiatric manifestations
CC associated with peripheral diseases including blood loss of any kind,
CC renal failure, conditions associated with anaemia, and neurological and

CC neuropsychiatric manifestations including haematological and
CC non-haematological malignancies/cancer, symptoms or complications in
CC patients receiving chemotherapy, inflammatory and infectious disorders
CC such as human immunodeficiency viral infections, and chronic systemic
CC autoimmune diseases such as systemic lupus erythematosus. The method is
CC also useful for prevention of plexopathies and neuropathies. This
CC sequence represents a human erythropoietin neuroprotective peptide of the
CC invention.

XX
SQ Sequence 20 AA;
Query Match 100.0%; Score 123; DB 23; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTASCHFGPLTWCKPQGG 20
|||||

RESULT 3
AAU13645
ID AAY13645 standard; peptide; 20 AA.
XX
AC AAY13645;
XX
DT 06-SEP-1999 (first entry)
XX
DE Erythropoietin receptor (EPO-R) binding peptide.
XX
KW Erythropoietin; EPO; receptor; EPO deficiency; renal failure; AIDS;
KW dialysis; anaemia; autoimmune disease; chronic inflammatory disease;
KW malignancy; beta-thalassaemia; cystic fibrosis; prematurity; blood loss;
KW spinal cord injury; aging; neoplastic disease; erythropoiesis; EPO-R.
XX
OS Synthetic.
XX
PN WO9640749-A1.
XX
PD 19-DEC-1996.
XX
PF 07-JUN-1996; 96WO-US09810.
XX
PR 07-JUN-1995; 95US-0484635.
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DR WPI; 1997-052225/05.
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CC the peptide may be cyclised or dimerised. The peptide can be used to
CC treat a patient having a disorder characterised by a deficiency of EPO
CC or a low or defective red blood cell population. It can be used to treat
CC end stage renal failure or dialysis; anaemia associated with AIDS,
CC autoimmune disease, chronic inflammatory diseases or malignancy;
CC beta-thalassaemia; cystic fibrosis; early anaemia of prematurity; spinal

CC cord injury; acute blood loss; aging; and neoplastic disease states
CC accompanied by abnormal erythropoiesis. The peptides can also be used as
CC reagents for detecting EPO receptors on living cells, in biological
CC fluids, in tissue homogenates, etc. Sequences AAY13624-661 represent
CC specific examples of EPO-R binding peptides.

XX
SQ Sequence 20 AA;
Query Match 96.7%; Score 119; DB 18; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.6e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTTSCHFGPLTWCKPQGG 20
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RESULT 4
AAU74477
ID AAU74477 standard; Peptide; 20 AA.
XX
AC AAU74477;
XX
DT 09-APR-2002 (first entry)
XX
DE Human erythropoietin neuroprotective peptide EMP-7.
XX
KW Neuroprotective peptide; human; erythropoietin; neurotoxicity; anaemia;
KW erythropoietin receptor; EPO receptor; neurodegeneration; prion disease;
KW neurological damage; neurodegenerative disorder; neurological disorder;
KW psychiatric disorder; blood loss; renal failure; cancer; HIV;
KW human immunodeficiency virus; haematology; autoimmune disease;
KW inflammatory disorder; infectious disease; EMP-7.
XX
OS Homo sapiens.
XX
PN WO200191780-A1.
XX
PD 06-DEC-2001.
XX
PF 23-MAY-2001; 2001WO-US16654.
XX
PR 26-MAY-2000; 2000US-207654P.
XX
PA (ORTH) ORTHO-MCNEIL PHARM INC.
PI Smith-Swintosky V, Renzi M, Plata-Salaman C, Jolliffe L, Farrell F;
PI Johnson DL;
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DR WPI; 2002-114307/15.
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PT neurodegeneration or neurological damage, involves administering to
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PS Claim 14; Page 41; 75pp; English.
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CC The invention relates to a method for treating a patient with a condition
CC mediated by neurotoxicity, neurodegeneration or neurological damage,
CC involving administering a peptide comprising one or more monomeric
CC peptides that bind to the human erythropoietin (EPO) receptor. The method
CC is useful for treating acute and chronic neurodegenerative disorders
CC including cerebral ischaemia or infarction, Alzheimer's disease, Pick's
CC disease, diffuse Lewy body disease, Shy-Drager syndrome, amyotrophic
CC lateral sclerosis, Huntington's disease, Parkinson's disease, Gilles De
CC La Tourette's disease, Tay-Sachs's disease, and prion diseases including
CC Creutzfeldt-Jakob and Kuru, neurological and psychiatric manifestations
CC associated with peripheral diseases including blood loss of any kind,
CC renal failure, conditions associated with anaemia, and neurological and
CC neuropsychiatric manifestations including haematological and
CC non-haematological malignancies/cancer, symptoms or complications in
CC patients receiving chemotherapy, inflammatory and infectious disorders

CC such as human immunodeficiency viral infections, and chronic systemic
 CC autoimmune diseases such as systemic lupus erythematosus. The method is
 CC also useful for prevention of plexopathies and neuropathies. This
 CC sequence represents a human erythropoietin neuroprotective peptide of the
 CC invention.

XX SQ Sequence 20 AA;

Query Match 96.7%; Score 119; DB 23; Length 20;
 Best Local Similarity 95.0%; Pred. No. 1.6e-09;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
 DB 1 GGTTSCHFGPLTWCKPQGG 20
 ||| ||||| ||||| ||||| |||||

RESULT 5
 AAU74485

ID AAU74485 standard; Peptide; 20 AA.

XX AC AAU74485;

DT 09-APR-2002 (first entry)

DE Human erythropoietin neuroprotective generic peptide (EMP-28-EMP-33).

XX KW Neuroprotective peptide; human; erythropoietin; neurotoxicity; anaemia;
 KW erythropoietin receptor; EPO receptor; neurodegeneration; prion disease;
 KW neurological damage; neurodegenerative disorder; neurological disorder;
 KW psychiatric disorder; blood loss; renal failure; cancer; HIV; EMP-32;
 KW human immunodeficiency virus; haematology; autoimmune disease; EMP-31;
 KW inflammatory disorder; infectious disease; EMP-28; EMP-29; EMP-30;
 KW EMP-33.

XX OS Homo sapiens.

FX Key Location/Qualifiers

FT Misc-difference 4 /note= "D-Tyr (EMP-28), p-NO 2-Phe (EMP-29), p-NH 2-Phe
 FT (EMP-30), p-F-Phe (EMP-31), p-I-Phe (EMP-32) or
 FT 3,5-dibromo-Tyr (EMP-33)"

VX WO2000191780-A1.

XX PD 06-DEC-2001.

XX PF 23-MAY-2001; 2001WO-US16654.

XX PR 26-MAY-2000; 2000US-207654P.

XX (ORTH) ORTHO-MCNEIL PHARM INC.

XX PI Smith-Swintosky V, Renzi M, Plata-Salaman C, Jolliffe L, Farrell F;
 PI Johnson DL;

XX DR WPI; 2002-114307/15.

XX PT Treating patients having condition mediated by neurotoxicity,
 PT neurodegeneration or neurological damage, involves administering to
 PT patient a peptide comprising monomeric peptides that bind to
 PT erythropoietin receptor -

XX PS Claim 14; Page 41; 75pp; English.

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 CC mediated by neurotoxicity, neurodegeneration or neurological damage,
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 CC is useful for treating acute and chronic neurodegenerative disorders
 CC including cerebral ischaemia or infarction, Alzheimer's disease, Pick's
 CC disease, diffuse Lewy body disease, Shy-Drager syndrome, amyotrophic
 CC lateral sclerosis, Huntington's disease, Parkinson's disease, Gilles De

CC La Tourette's disease, Tay-Sach's disease, and prion diseases including
 CC Creutzfeldt-Jakob and Kuru, neurological and psychiatric manifestations
 CC associated with peripheral diseases including blood loss of any kind,
 CC renal failure, conditions associated with anaemia, and neurological and
 CC neuropsychiatric manifestations including haematological and
 CC non-haematological malignancies/cancer, symptoms or complications in
 CC patients receiving chemotherapy, inflammatory and infectious disorders
 CC such as human immunodeficiency viral infections, and chronic systemic
 CC autoimmune diseases such as systemic lupus erythematosus. The method is
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 CC invention.

XX SQ Sequence 20 AA;

Query Match 96.7%; Score 119; DB 23; Length 20;
 Best Local Similarity 95.0%; Pred. No. 1.6e-09;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
 DB 1 GGTXSCHFGPLTWCKPQGG 20
 ||| ||||| ||||| ||||| |||||

RESULT 6
 AAY26550

ID AAY26550 standard; peptide; 20 AA.

XX AC AAY26550;

DT 06-SEP-1999 (first entry)

XX DE Erythropoietin receptor (EPO-R) binding peptide.

XX KW Erythropoietin; EPO; receptor; EPO deficiency; renal failure; AIDS;
 KW dialysis; anaemia; autoimmune disease; chronic inflammatory disease;
 KW malignancy; beta-thalassaemia; cystic fibrosis; prematurity; blood loss;
 KW spinal cord injury; aging; neoplastic disease; erythropoiesis; EPO-R.

XX OS Synthetic.

XX PN WO9640749-A1.

XX PD 19-DEC-1996.

XX PF 07-JUN-1996; 96WO-US09810.

XX PR 07-JUN-1995; 95US-0484635.

XX PR 07-JUN-1995; 95US-0484631.

XX PR 19-NOV-1993; 93US-0155940.

XX (AFFY-) AFFYMAX TECHNOLOGIES NV.
 (JOHJ) JOHNSON & JOHNSON CORP.
 (ORTH) ORTHO PHARM CORP.

XX PI Chang RS, Dower WJ, Johnson D, Jolliffe LK, Kashyap AK;
 PI Mulcahy L, Wrighton NC;

XX DR WPI; 1997-052225/05.

XX PT Erythropoietin receptor binding peptide - useful for treating
 PT disorders characterised by deficiency of EPO, or low or defective
 PT red blood cell population

XX PS Disclosure; Page 28; 95pp; English.

XX CC The invention describes a peptide of 10-40 amino acid residues which
 CC binds to erythropoietin (EPO) receptor and which includes the amino acid
 CC sequence Cys-Xaa1-Xaa2-Gly-Pro-Xaa3-Thr-Trp-Xaa4-Cys, where Xaa1 = Arg,
 CC His, Leu or Trp, Xaa2 = Met, Phe or Ile, Xaa3 = 1 of the 20 Genetically
 CC coded L-amino acids, and Xaa4 = Asp, Glu, Ile, Leu or Val. Optionally,
 CC the peptide may be cyclised or dimerised. The peptide can be used to
 CC treat a patient having a disorder characterised by a deficiency of EPO

CC cord injury; acute blood loss; aging; and neoplastic disease states
CC accompanied by abnormal erythropoiesis. The peptides can also be used as
CC reagents for detecting EPO receptors on living cells, in biological
CC fluids, in tissue homogenates, etc. Sequences AAY26352-548 are
CC representative peptides falling within the above peptide motif and
CC isolated during the affinity selection process.

XX
SQ Sequence 20 AA;

Query Match 95.1%; Score 117; DB 18; Length 20;
Best Local Similarity 95.0%; Pred. No. 3.1e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| ||||| ||||| |||||
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 4
AAY26387
ID AAY26387 standard; peptide; 20 AA.
XX
AC AAY26387;
XX
DT 06-SEP-1999 (first entry)
XX
DE Erythropoietin receptor (EPO-R) binding peptide.
XX
DE Erythropoietin; EPO; receptor; EPO deficiency; renal failure; AIDS;
XX dialysis; anaemia; autoimmune disease; chronic inflammatory disease;
KW malignancy; beta-thalassaemia; cystic fibrosis; prematurity; blood loss;
KW spinal cord injury; aging; neoplastic disease; erythropoiesis; EPO-R.
XX
OS Synthetic.
XX
PN WO9640749-A1.
XX
PD 19-DEC-1996.
XX
PF 07-JUN-1996; 96WO-US09810.
XX
PR 07-JUN-1995; 95US-0484635.
PR 07-JUN-1995; 95US-0484631.
PR 19-NOV-1993; 93US-0155940.
XX
PA (AFFY-) AFFYMAX TECHNOLOGIES NV.
PA (JOHJ) JOHNSON & JOHNSON CORP.
PA (ORTH) ORTHO PHARM CORP.
XX
PI Chang RS, Dower WJ, Johnson D, Jolliffe LK, Kashyap AK;
PI Mulcahy L, Wrighton NC;
XX
DR WPI; 1997-052225/05.
XX
PT Erythropoietin receptor binding peptide - useful for treating
PT disorders characterised by deficiency of EPO, or low or defective
PT red blood cell population
XX
PS Disclosure; Page 17; 95pp; English.
XX
CC The invention describes a peptide of 10-40 amino acid residues which
CC binds to erythropoietin (EPO) receptor and which includes the amino acid
CC sequence Cys-Xaa1-Xaa2-Gly-Pro-Xaa3-Thr-Trp-Xaa4-Cys, where Xaa1 = Arg,
CC His, Leu or Trp, Xaa2 = Met, Phe or Ile, Xaa3 = 1 of the 20 genetically
CC coded L-amino acids, and Xaa4 = Asp, Glu, Ile, Leu or Val. Optionally,
CC the peptide may be cyclised or dimerised. The peptide can be used to
CC treat a patient having a disorder characterised by a deficiency of EPO
CC or a low or defective red blood cell population. It can be used to treat
CC end stage renal failure or dialysis; anaemia associated with AIDS,
CC autoimmune disease, chronic inflammatory diseases or malignancy;
CC beta-thalassaemia; cystic fibrosis; early anaemia of prematurity; spinal
CC cord injury; acute blood loss; aging; and neoplastic disease states
CC accompanied by abnormal erythropoiesis. The peptides can also be used as

CC reagents for detecting EPO receptors on living cells, in biological
CC fluids, in tissue homogenates, etc. Sequences AAY26352-548 are
CC representative peptides falling within the above peptide motif and
CC isolated during the affinity selection process.

XX
SQ Sequence 20 AA;

Query Match 95.1%; Score 117; DB 18; Length 20;
Best Local Similarity 95.0%; Pred. No. 3.1e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| ||||| ||||| |||||
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 10
AAY26399
ID AAY26399 standard; peptide; 20 AA.
XX
AC AAY26399;
XX
DT 06-SEP-1999 (first entry)
XX
DE Erythropoietin receptor (EPO-R) binding peptide.
XX
DE Erythropoietin; EPO; receptor; EPO deficiency; renal failure; AIDS;
XX dialysis; anaemia; autoimmune disease; chronic inflammatory disease;
KW malignancy; beta-thalassaemia; cystic fibrosis; prematurity; blood loss;
KW spinal cord injury; aging; neoplastic disease; erythropoiesis; EPO-R.
XX
OS Synthetic.
XX
PN WO9640749-A1.
XX
PD 19-DEC-1996.
XX
PF 07-JUN-1996; 96WO-US09810.
XX
PR 07-JUN-1995; 95US-0484635.
PR 07-JUN-1995; 95US-0484631.
PR 19-NOV-1993; 93US-0155940.
XX
PA (AFFY-) AFFYMAX TECHNOLOGIES NV.
PA (JOHJ) JOHNSON & JOHNSON CORP.
PA (ORTH) ORTHO PHARM CORP.
XX
PI Chang RS, Dower WJ, Johnson D, Jolliffe LK, Kashyap AK;
PI Mulcahy L, Wrighton NC;
XX
DR WPI; 1997-052225/05.
XX
PT Erythropoietin receptor binding peptide - useful for treating
PT disorders characterised by deficiency of EPO, or low or defective
PT red blood cell population
XX
PS Disclosure; Page 18; 95pp; English.
XX
CC The invention describes a peptide of 10-40 amino acid residues which
CC binds to erythropoietin (EPO) receptor and which includes the amino acid
CC sequence Cys-Xaa1-Xaa2-Gly-Pro-Xaa3-Thr-Trp-Xaa4-Cys, where Xaa1 = Arg,
CC His, Leu or Trp, Xaa2 = Met, Phe or Ile, Xaa3 = 1 of the 20 genetically
CC coded L-amino acids, and Xaa4 = Asp, Glu, Ile, Leu or Val. Optionally,
CC the peptide may be cyclised or dimerised. The peptide can be used to
CC treat a patient having a disorder characterised by a deficiency of EPO
CC or a low or defective red blood cell population. It can be used to treat
CC end stage renal failure or dialysis; anaemia associated with AIDS,
CC autoimmune disease, chronic inflammatory diseases or malignancy;
CC beta-thalassaemia; cystic fibrosis; early anaemia of prematurity; spinal
CC cord injury; acute blood loss; aging; and neoplastic disease states
CC accompanied by abnormal erythropoiesis. The peptides can also be used as
CC reagents for detecting EPO receptors on living cells, in biological
CC fluids, in tissue homogenates, etc. Sequences AAY26352-548 are

CC representative peptides falling within the above peptide motif and
XX isolated during the affinity selection process.

SQ Sequence 20 AA;

Query Match 95.1%; Score 117; DB 18; Length 20;
Best Local Similarity 95.0%; Pred. No. 3.1e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| ||||| ||||| |||||
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 11
AAY26372
ID AAY26372 standard; peptide; 20 AA.
XX
AC AAY26372;
XX
DT 06-SEP-1999 (first entry)
XX
DE Erythropoietin receptor (EPO-R) binding peptide.
XX
KW Erythropoietin; EPO; receptor; EPO deficiency; renal failure; AIDS;
KW dialysis; anaemia; autoimmune disease; chronic inflammatory disease;
KW malignancy; beta-thalassaemia; cystic fibrosis; prematurity; blood loss;
KW spinal cord injury; aging; neoplastic disease; erythropoiesis; EPO-R.
XX
OS Synthetic.
XX
PN WO9640749-A1.
XX
PD 19-DEC-1996.
XX
PF 07-JUN-1996; 96WO-US09810.
XX
PR 07-JUN-1995; 95US-0484635.
PR 07-JUN-1995; 95US-0484631.
PR 19-NOV-1993; 93US-0155940.
XX
PA (AFFY-) AFFYMAX TECHNOLOGIES NV.
PA (JOHJ) JOHNSON & JOHNSON CORP.
PA (ORTH) ORTHO PHARM CORP.
XX
PI Chang RS, Dower WJ, Johnson D, Jolliffe LK, Kashyap AK;
PI Mulcahy L, Wrighton NC;
XX
DR WPI; 1997-052225/05.
XX
PT Erythropoietin receptor binding peptide - useful for treating
PT disorders characterised by deficiency of EPO, or low or defective
PT red blood cell population
XX
PS Disclosure; Page 16; 95pp; English.

CC The invention describes a peptide of 10-40 amino acid residues which
CC binds to erythropoietin (EPO) receptor and which includes the amino acid
CC sequence Cys-Xaa1-Xaa2-Gly-Pro-Xaa3-Thr-Trp-Xaa4-Cys, where Xaa1 = Arg,
CC His, Leu or Trp, Xaa2 = Met, Phe or Ile, Xaa3 = 1 of the 20 genetically
CC coded L-amino acids, and Xaa4 = Asp, Glu, Ile, Leu or Val. Optionally,
CC the peptide may be cyclised or dimerised. The peptide can be used to
CC treat a patient having a disorder characterised by a deficiency of EPO
CC or a low or defective red blood cell population. It can be used to treat
CC end stage renal failure or dialysis; anaemia associated with AIDS,
CC autoimmune disease, chronic inflammatory diseases or malignancy;
CC beta-thalassaemia; cystic fibrosis; early anaemia of prematurity; spinal
CC cord injury; acute blood loss; aging; and neoplastic disease states
CC accompanied by abnormal erythropoiesis. The peptides can also be used as
CC reagents for detecting EPO receptors on living cells, in biological
CC fluids, in tissue homogenates, etc. Sequences AAY26352-548 are
CC representative peptides falling within the above peptide motif and
CC isolated during the affinity selection process.

XX
SQ Sequence 20 AA;

Query Match 95.1%; Score 117; DB 18; Length 20;
Best Local Similarity 95.0%; Pred. No. 3.1e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| ||||| ||||| |||||
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 12
AAY13646
ID AAY13646 standard; peptide; 20 AA.
XX
AC AAY13646;
XX
DT 06-SEP-1999 (first entry)
XX
DE Erythropoietin receptor (EPO-R) binding peptide.
XX
KW Erythropoietin; EPO; receptor; EPO deficiency; renal failure; AIDS;
KW dialysis; anaemia; autoimmune disease; chronic inflammatory disease;
KW malignancy; beta-thalassaemia; cystic fibrosis; prematurity; blood loss;
KW spinal cord injury; aging; neoplastic disease; erythropoiesis; EPO-R.
XX
OS Synthetic.
XX
PN WO9640749-A1.
XX
PD 19-DEC-1996.
XX
PF 07-JUN-1996; 96WO-US09810.
XX
PR 07-JUN-1995; 95US-0484635.
PR 07-JUN-1995; 95US-0484631.
PR 19-NOV-1993; 93US-0155940.
XX
PA (AFFY-) AFFYMAX TECHNOLOGIES NV.
PA (JOHJ) JOHNSON & JOHNSON CORP.
PA (ORTH) ORTHO PHARM CORP.
XX
PI Chang RS, Dower WJ, Johnson D, Jolliffe LK, Kashyap AK;
PI Mulcahy L, Wrighton NC;
XX
DR WPI; 1997-052225/05.
XX
PT Erythropoietin receptor binding peptide - useful for treating
PT disorders characterised by deficiency of EPO, or low or defective
PT red blood cell population
XX
PS Claim 6; Page 68; 95pp; English.

CC The invention describes a peptide of 10-40 amino acid residues which
CC binds to erythropoietin (EPO) receptor and which includes the amino acid
CC sequence Cys-Xaa1-Xaa2-Gly-Pro-Xaa3-Thr-Trp-Xaa4-Cys, where Xaa1 = Arg,
CC His, Leu or Trp, Xaa2 = Met, Phe or Ile, Xaa3 = 1 of the 20 genetically
CC coded L-amino acids, and Xaa4 = Asp, Glu, Ile, Leu or Val. Optionally,
CC the peptide may be cyclised or dimerised. The peptide can be used to
CC treat a patient having a disorder characterised by a deficiency of EPO
CC or a low or defective red blood cell population. It can be used to treat
CC end stage renal failure or dialysis; anaemia associated with AIDS,
CC autoimmune disease, chronic inflammatory diseases or malignancy;
CC beta-thalassaemia; cystic fibrosis; early anaemia of prematurity; spinal
CC cord injury; acute blood loss; aging; and neoplastic disease states
CC accompanied by abnormal erythropoiesis. The peptides can also be used as
CC reagents for detecting EPO receptors on living cells, in biological
CC fluids, in tissue homogenates, etc. Sequences AAY13624-661 represent
CC specific examples of EPO-R binding peptides.

XX
SQ Sequence 20 AA;

Query Match 95.1%; Score 117; DB 18; Length 20;
Best Local Similarity 95.0%; Pred. No. 3.1e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTASCHFGPLTWCKPQGG 20

RESULT 13
AAV13683
ID AAV13683 standard; peptide; 20 AA.
XX
AC AAV13683;
XX
DT 06-SEP-1999 (first entry)
XX
DE Erythropoietin receptor (EPO-R) binding peptide.
XX
KW Erythropoietin; EPO; receptor; EPO deficiency; renal failure; AIDS;
KW dialysis; anaemia; autoimmune disease; chronic inflammatory disease;
KW malignancy; beta-thalassaemia; cystic fibrosis; prematurity; blood loss;
KW spinal cord injury; aging; neoplastic disease; erythropoiesis; EPO-R.
XX
OS Synthetic.
XX WO9640749-A1.
XX
PD 19-DEC-1996.
XX
PF 07-JUN-1996; 96WO-US09810.
XX
PR 07-JUN-1995; 95US-0484635.
PR 07-JUN-1995; 95US-0484631.
PR 19-NOV-1993; 93US-0155940.
XX
PA (AFFY-) AFFYMAX TECHNOLOGIES NV.
PA (JOHJ) JOHNSON & JOHNSON CORP.
PA (ORTH) ORTHO PHARM CORP.
XX
PI Chang RS, Dower WJ, Johnson D, Jolliffe LK, Kashyap AK;
PI Mulcahy L, Wrighton NC;
XX
DR WPI; 1997-052225/05.
XX
PT Erythropoietin receptor binding peptide - useful for treating
PT disorders characterised by deficiency of EPO, or low or defective
PT red blood cell population
XX
PS Disclosure; Fig 2; 95pp; English.
XX
CC The invention describes a peptide of 10-40 amino acid residues which
CC binds to erythropoietin (EPO) receptor and which includes the amino acid
CC sequence Cys-Xaa1-Xaa2-Gly-Pro-Xaa3-Thr-Trp-Xaa4-Cys, where Xaa1 = Arg,
CC His, Leu or Trp, Xaa2 = Met, Phe or Ile, Xaa3 = 1 of the 20 genetically
CC coded L-amino acids, and Xaa4 = Asp, Glu, Ile, Leu or Val. Optionally,
CC the peptide may be cyclised or dimerised. The peptide can be used to
CC treat a patient having a disorder characterised by a deficiency of EPO
CC or a low or defective red blood cell population. It can be used to treat
CC end stage renal failure or dialysis; anaemia associated with AIDS,
CC autoimmune disease, chronic inflammatory diseases or malignancy;
CC beta-thalassaemia; cystic fibrosis; early anaemia of prematurity; spinal
CC cord injury; acute blood loss; aging; and neoplastic disease states
CC accompanied by abnormal erythropoiesis. The peptides can also be used as
CC reagents for detecting EPO receptors on living cells, in biological
CC fluids, in tissue homogenates, etc. Sequences AAV13662-735 are
CC representative peptides of the invention.
XX
SQ Sequence 20 AA;

Query Match 95.1%; Score 117; DB 18; Length 20;
Best Local Similarity 95.0%; Pred. No. 3.1e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTASCHFGPLTWCKPQGG 20

RESULT 14
AAW43020
ID AAW43020 standard; peptide; 20 AA.
XX
AC AAW43020;
XX
DT 05-MAY-1998 (first entry)
XX
DE Peptide mimetic of erythropoietin.
XX
KW EMPI; peptide mimetic; erythropoietin; EPO; mimic; EPO-receptor;
KW 3-dimensional co-ordinate; atom subset; extracellular domain;
KW criteria data set; CDS; agonist; EPO activity; treatment; anaemia.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 6..15
XX
PN WO9741526-A1.
XX
PD 06-NOV-1997.
XX
PF 28-APR-1997; 97WO-US07218.
XX
PR 26-APR-1996; 96US-0641071.
XX
PA (SCRI) SCRIPPS RES INST.
XX
PI Johnson DL, Jolliffe LK, Livnah O, Stura EA, Wilson IA;
XX
DR WPI; 1997-549970/50.
XX
PT Identifying potential mimics of erythropoietin for treating anaemia
PT - using computer analysis of coordinates of the complex of
PT erythropoietin receptor domain with a known peptide mimic
XX
PS Claim 1; Page 79; 85pp; English.
XX
CC The present peptide, EMPI, is a peptide mimetic of erythropoietin (EPO).
CC EPO is the primary regulator of proliferation and differentiation of
CC immature erythroid cells. EMPI competes with EPO in receptor binding
CC assays, and induces cellular proliferation of cell lines engineered to
CC be responsive to EPO. Further, EMPI demonstrates significant
CC erythropoietic effects in mice. The sequence of EMPI is unrelated to EPO.
CC Potential mimics of EPO are identified by supplying a computer with
CC 3-dimensional co-ordinates of a subset of atoms in EMPI when this has
CC been co-crystallised with the 1-225 amino acid fragment (the
CC extracellular domain) of the EPO-receptor, to generate a criteria data
CC set (CDS). The computer then compares the CDS with a database of chemical
CC structures and those structures with a portion structurally similar to
CC CDS are selected and displayed. Alternatively, the computer constructs a
CC model of a chemical structure having a portion structurally similar to
CC CDS and displays it. The EPO mimics are agonists of the EPO-receptor in
CC in vivo or in vitro tests of EPO activity. They are potentially useful in
CC the treatment of anaemia caused by chronic renal failure, cancer
CC chemotherapy or treatment with azidothymidine.
XX
SQ Sequence 20 AA;

Query Match 95.1%; Score 117; DB 18; Length 20;
Best Local Similarity 95.0%; Pred. No. 3.1e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 15

AAW26963
ID AAW26963 standard; peptide; 20 AA.

XX AC AAW26963;

XX 10-NOV-1997 (first entry)

DE Monomer subunit of erythropoietin receptor binding dimer.

XX Monomer; erythropoietin; EPO; receptor; binding; dimer; activation;
KW treatment; disorder; deficiency; low; defective; red blood cell;
KW erythrocyte; population; cell surface; agonist; end stage; renal;
KW failure; dialysis; anaemia; anemia; AIDS; chronic;
KW inflammatory; disease; rheumatoid arthritis; bowel inflammation;
KW autoimmune; transfusion.

XX Synthetic.

XX WO9640772-A2.

XX 19-DEC-1996.

XX 06-JUN-1996; 96WO-US09469.

XX 07-JUN-1995; 95US-0484135.

XX (ORTH) ORTHO PHARM CORP.

XX (JOHJ) JOHNSON & JOHNSON.

XX Johnson DL, Zivin RA;

XX WPI; 1997-099920/09.

XX Activating cell surface receptors using peptide dimer agonists -
PT also, new dimers of erythropoietin receptor binding peptide(s)
PT useful for treating patient having disorder characterised by EPO
PT deficiency

XX Claim 6; Page 93; 110pp; English.

XX The present peptide is a monomer subunit of an erythropoietin (EPO)
CC receptor binding dimer, which comprises 2 EPO receptor binding
CC monomers of 10 to 40 amino acids, and activates or improves the
CC bioactivity of the EPO cell surface receptor. The dimer can be used
CC to treat disorders resulting from EPO deficiency by improving the
CC activity of its cell surface receptor, e.g. end stage renal
CC failure/dialysis, anaemia associated with AIDS or chronic
CC inflammatory diseases such as rheumatoid arthritis and chronic
CC bowel inflammation and autoimmune disease. It can also be used to
CC boost the red cell count of a patient prior to surgery or as
CC pretreatment to transfusion. The dimer peptide exhibits increased
CC biological potency in vitro and in vivo relative to its component
CC monomeric agonists. Dimerisation may also convert cell surface
CC receptor antagonists into agonists.

XX Sequence 20 AA;

Query Match 95.1%; Score 117; DB 18; Length 20;
Best Local Similarity 95.0%; Pred. No. 3.1e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20

Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 16

AAW26975
ID AAW26975 standard; peptide; 20 AA.

XX

AC AAW26975;

XX 11-NOV-1997 (first entry)

XX Monomer subunit of erythropoietin receptor binding dimer.

XX Monomer; erythropoietin; EPO; receptor; binding; dimer; activation;
KW treatment; disorder; deficiency; low; defective; red blood cell;
KW erythrocyte; population; cell surface; agonist; end stage; renal;
KW failure; dialysis; anaemia; anemia; AIDS; chronic;
KW inflammatory; disease; rheumatoid arthritis; bowel inflammation;
KW autoimmune; transfusion.

XX Synthetic.

XX Key Location/Qualifiers

XX Modified-site 1

XX /note= "acylated"

XX WO9640772-A2.

XX 19-DEC-1996.

XX 06-JUN-1996; 96WO-US09469.

XX 07-JUN-1995; 95US-0484135.

XX (ORTH) ORTHO PHARM CORP.

XX (JOHJ) JOHNSON & JOHNSON.

XX Johnson DL, Zivin RA;

XX WPI; 1997-099920/09.

XX Activating cell surface receptors using peptide dimer agonists -
PT also, new dimers of erythropoietin receptor binding peptide(s)
PT useful for treating patient having disorder characterised by EPO
PT deficiency

XX Example 5; Fig 9; 110pp; English.

XX The present peptide is a specific example of a claimed generic
CC monomer subunit of an erythropoietin (EPO) receptor binding dimer,
CC which comprises 2 EPO receptor binding monomers of 10 to 40 amino
CC acids, and activates or improves the bioactivity of the EPO cell
CC surface receptor. The dimer can be used to treat disorders
CC resulting from EPO deficiency by improving the activity of its
CC cell surface receptor, e.g. end stage renal failure/dialysis,
CC anaemia associated with AIDS or chronic inflammatory diseases such
CC as rheumatoid arthritis and chronic bowel inflammation and
CC autoimmune disease. It can also be used to boost the red cell
CC count of a patient prior to surgery or as pretreatment to
CC transfusion. The dimer peptide exhibits increased biological
CC potency in vitro and in vivo relative to its component monomeric
CC agonists. Dimerisation may also convert cell surface receptor
CC antagonists into agonists.

XX Sequence 20 AA;

Query Match 95.1%; Score 117; DB 18; Length 20;
Best Local Similarity 95.0%; Pred. No. 3.1e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20

Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 17

AAW26997
ID AAW26997 standard; peptide; 20 AA.

XX

AC AAW26997;

XX 11-NOV-1997 (first entry)
DT
XX
DE Monomer subunit of erythropoietin receptor binding dimer.
XX
KW Monomer; erythropoietin; EPO; receptor; binding; dimer; activation;
KW treatment; disorder; deficiency; low; defective; red blood cell;
KW erythrocyte; population; cell surface; agonist; end stage; renal;
KW failure; dialysis; anaemia; anemia; AIDS; chronic;
KW inflammatory; disease; rheumatoid arthritis; bowel inflammation;
KW autoimmune; transfusion.
XX
OS Synthetic.
XX
PN WO9640772-A2.
XX
PD 19-DEC-1996.
XX
PF 06-JUN-1996; 96WO-US09469.
XX
XX 07-JUN-1995; 95US-0484135.
PR
XX (ORTH) ORTHO PHARM CORP.
PA (JOHN) JOHNSON & JOHNSON.
XX
XX Johnson DL, Zivin RA;
PI WPI; 1997-099920/09.
XX
XX Activating cell surface receptors using peptide dimer agonists -
PT also, new dimers of erythropoietin receptor binding peptide(s)
PT useful for treating patient having disorder characterised by EPO
PT deficiency
XX
PS Disclosure; Fig 9; 110pp; English.
XX
XX The present peptide is a specific example of a claimed generic
CC monomer subunit of an erythropoietin (EPO) receptor binding dimer,
CC which comprises 2 EPO receptor binding monomers of 10 to 40 amino
CC acids, and activates or improves the bioactivity of the EPO cell
CC surface receptor. The dimer can be used to treat disorders
CC resulting from EPO deficiency by improving the activity of its
CC cell surface receptor, e.g. end stage renal failure/dialysis,
CC anaemia associated with AIDS or chronic inflammatory diseases such
CC as rheumatoid arthritis and chronic bowel inflammation and
CC autoimmune disease. It can also be used to boost the red cell
CC count of a patient prior to surgery or as pretreatment to
CC transfusion. The dimer peptide exhibits increased biological
CC potency in vitro and in vivo relative to its component monomeric
CC agonists. Dimerisation may also convert cell surface receptor
CC antagonists into agonists.
XX
SQ Sequence 20 AA;
Query Match 95.1%; Score 117; DB 18; Length 20;
Best Local Similarity 95.0%; Pred. No. 3.1e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTYSCHFGLTWCKPQGG 20
RESULT 18
AAB13501
ID AAB13501 standard; peptide; 20 AA.
XX
AC AAB13501;
XX
DT 02-NOV-2000 (first entry)
XX
DE Erythropoietin derived peptide #2.
XX

KW Erythropoietin derivative; diagnostic agent; therapeutic agent.
XX Unidentified.
OS
XX US6077939-A.
PN
XX 20-JUN-2000.
PD
XX 04-AUG-1997; 97US-0905310.
PF
XX 04-AUG-1997; 97US-0905310.
PR
XX (ORTH) ORTHO-MCNEIL PHARM INC.
PA
XX Wei Z, Ghosh-Dastidar P, Menon-Rudolph S;
PI WPI; 2000-450981/39.
XX
XX Covalently binding a water-soluble polymer to the N-terminal
PT alpha-carbon atom of a polypeptide for producing therapeutic and
PT diagnostic agents, by contacting the transaminated polypeptide with the
PT polymer to form a hydrazone bond -
XX
PS Disclosure; Column 5; 21pp; English.
XX
XX The present sequence is a peptide derivative of erythropoietin. It can be
CC used in the method of the invention, which involves the production of
CC compositions comprising a polypeptide with a water soluble polymer
CC covalently bound to the N-terminal alpha carbon by a hydrazone or an
CC oxime (or the reduced version of each) bond. This is useful as previous
CC methods were more time consuming and labour-intensive, as well as being
CC less precise. The composition can be used to produce diagnostic and
CC therapeutic agents.
XX
SQ Sequence 20 AA;
Query Match 95.1%; Score 117; DB 21; Length 20;
Best Local Similarity 95.0%; Pred. No. 3.1e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTYSCHFGLTWCKPQGG 20
RESULT 19
AAB17031
ID AAB17031 standard; Peptide; 20 AA.
XX
AC AAB17031;
XX
DT 31-OCT-2000 (first entry)
XX
DE EPO-mimetic peptide sequence SEQ ID NO:87.
XX
KW Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist;
KW MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
KW vascular endothelial growth factor; matrix metalloproteinase;
KW asthma; thrombosis; pharmaceutical.
XX
OS Synthetic.
XX
PN WO200024782-A2.
XX
PD 04-MAY-2000.
XX
PF 25-OCT-1999; 99WO-US25044.
XX
PR 23-OCT-1998; 98US-0105371.
PR 22-OCT-1999; 99US-0428082.

XX (AMGE-) AMGEN INC.
XX Feige U, Liu C, Cheetham J, Boone TC;
PI WPI; 2000-350702/30.
XX
DR Novel composition of matter comprising an Fc domain and
XX pharmacologically active peptides, useful for treating cancer and
PT autoimmune diseases -
PT
XX Claim 13; Page 224; 608pp; English.
PS
XX The present invention describes composition of matter (I) comprising an
XX Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2,
CC -(L1)c-P1-(L2)d-P2-(L3)e-P³, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
CC where P1, P2, P3, and P4 = are each independently sequences of
CC pharmacologically active peptides; L1, L2, L3, and L4 = are each
CC independently linkers; and a, b, c, d, e, and f = are each independently
CC 0 or 1, provided that at least 1 of a and b is 1. The composition can
CC have cytostatic, antiasthmatic, thrombolytic and immunosuppressive
CC activities. DNAs, vectors and host cells from the present invention can
CC be used for producing pharmaceutical compositions. The compositions are
CC useful for treating cancer, asthma, thrombosis, or autoimmune diseases.
CC The use of an Fc domain (rather than a Fab domain) can provide a longer
CC half-life or incorporate functions such as Fc receptor binding, protein
CC A binding, complement fixation, and possibly placental transfer. AAA69443
CC to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid
CC sequences used in the exemplification of the present invention.
XX
SQ Sequence 20 AA;
Query Match 95.1%; Score 117; DB 21; Length 20;
Best Local Similarity 95.0%; Pred. No. 3.1e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTYSCHFGPLTWCKPQGG 20
||| |||||
RESULT 20
AAB17921
ID AAB17921 standard; Peptide; 20 AA.
XX
AC AAB17921;
XX
DT 31-OCT-2000 (first entry)
XX
DE EPO-mimetic peptide sequence SEQ ID NO:1025.
XX
KW Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist;
KW MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
KW vascular endothelial growth factor; matrix metalloproteinase;
KW asthma; thrombosis; pharmaceutical.
XX
OS Synthetic.
XX
PN WO200024782-A2.
XX
PD 04-MAY-2000.
XX
PF 25-OCT-1999; 99WO-US25044.
XX
XX 23-OCT-1998; 98US-0105371.
PR 22-OCT-1999; 99US-0428082.
XX
PA (AMGE-) AMGEN INC.

XX Feige U, Liu C, Cheetham J, Boone TC;
XX WPI; 2000-350702/30.
DR
XX
PT Novel composition of matter comprising an Fc domain and
PT pharmacologically active peptides, useful for treating cancer and
PT autoimmune diseases -
XX Claim 13; Page 556; 608pp; English.
XX
CC The present invention describes composition of matter (I) comprising an
CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2,
CC -(L1)c-P1-(L2)d-P2-(L3)e-P³, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
CC where P1, P2, P3, and P4 = are each independently sequences of
CC pharmacologically active peptides; L1, L2, L3, and L4 = are each
CC independently linkers; and a, b, c, d, e, and f = are each independently
CC 0 or 1, provided that at least 1 of a and b is 1. The composition can
CC have cytostatic, antiasthmatic, thrombolytic and immunosuppressive
CC activities. DNAs, vectors and host cells from the present invention can
CC be used for producing pharmaceutical compositions. The compositions are
CC useful for treating cancer, asthma, thrombosis, or autoimmune diseases.
CC The use of an Fc domain (rather than a Fab domain) can provide a longer
CC half-life or incorporate functions such as Fc receptor binding, protein
CC A binding, complement fixation, and possibly placental transfer. AAA69443
CC to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid
CC sequences used in the exemplification of the present invention.
XX
SQ Sequence 20 AA;
Query Match 95.1%; Score 117; DB 21; Length 20;
Best Local Similarity 95.0%; Pred. No. 3.1e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTYSCHFGPLTWCKPQGG 20
||| |||||
RESULT 21
AAG63738
ID AAG63738 standard; peptide; 20 AA.
XX
AC AAG63738;
XX
DT 29-OCT-2001 (first entry)
XX
DE Peptide agonist for the erythropoietin receptor (EPO-R).
XX
KW Insulin-like growth factor; IGF; IGF-1; IGF binding protein; IGFBP;
KW hyperglycemic disorder; obesity-related disorder; neurological disorder;
KW cardiac disorder; anabolic disorder; renal disorder; neuroprotection;
KW immunological disorder; kidney regeneration; degenerative disorder;
KW hypoxia; wound healing; cardiac regeneration; cancer; angiogenesis;
KW metabolic stress; growth hormone deficiency; diabetes; short stature;
KW osteoporosis; obesity; erythropoietin receptor.
XX
OS Unidentified.
XX
PN US6251865-B1.
XX
PD 26-JUN-2001.
XX
PF 31-MAR-1998; 98US-0052888.
XX
PR 04-APR-1997; 97US-0825852.
XX
PA (GETH) GENENTECH INC.
XX
PI Clark RG, Lowman HB, Robinson ICAF;
XX

DR WPI; 2001-520042/57.

XX Isolated peptides used to increase serum and tissue levels of

PT insulin-like growth factor in those with hyperglycemic,

PT obesity-related, neurological, cardiac, anabolic, renal or

PT immunological disorders -

XX

PS Example 7; Column 53; 108pp; English.

XX

CC The present sequence is an agonist for the erythropoietin receptor.

CC The specification describes insulin-like growth factor (IGF)-1 agonists,

CC which are used to increase serum and tissue levels of IGF-1 in mammals

CC with hyperglycemic, obesity-related, neurological, cardiac, anabolic,

CC renal or immunological disorders. They may also be used to increase whole

CC body, bone and muscle growth rate in normal and hypopituitary animals,

CC to protect body weight and nitrogen loss during catabolic states,

CC kidney regeneration, to treat peripheral and central nervous system

CC (CNS) degenerative disorders and promote neuroprotection or repair

CC following CNS damage or injury, to treat hypoxia, to promote wound

CC healing, for cardiac regeneration, to reverse cancer cachexia, to

CC inhibit angiogenesis, to regenerate the gastrointestinal tract, to

CC stimulate mammary function, to counteract IGF-1-dependent actions of

CC growth hormone such as metabolic stress, age-related decline in growth

CC hormone activity and adult growth hormone deficiency, to treat maturity

CC onset diabetes and/or to treat specific IGF deficiency. They may also

CC be used to treat growth-hormone resistant short stature, growth hormone

CC insensitivity syndrome, osteoporosis and catabolic states, and reduce

CC obesity.

XX

SQ Sequence 20 AA;

Query Match 95.1%; Score 117; DB 22; Length 20;

Best Local Similarity 95.0%; Pred. No. 3.1e-09;

Matches 19; Conservative 0; Mismatches 1; Indels 3; Gaps 0;

QY 1 GGTASCHFGPLTWVCKPQGG 20

Db 1 GGTYSCHFGPLTWVCKPQGG 20

PELUT 22

AAB97489

ID AAB97489 standard; peptide; 20 AA.

XX

AC AAB97489;

XX

DT 03-AUG-2001 (first entry)

XX

DE Erythropoietin cyclic mimetic peptide #1.

XX

KW Erythropoietin; mimetic; EPO; cyclic; EPO binding protein; EBP;

KW drug discovery.

XX

OS Synthetic.

XX

PN US6221608-B1.

XX

PD 24-APR-2001.

XX

PF 22-JAN-1997; 97US-0786690.

XX

PR 22-JAN-1997; 97US-0786690.

XX

PA (ORTH) ORTHO PHARM CORP.

XX

PI Middleton SA, Johnson D, McMahon FJ, Mulkahy LS, Jolliffe LK;

XX

FT Key Location/Qualifiers

FT Disulfide-bond 6..15

FT /note= "disulfide bond cyclizes the molecule"

FT Modified-site 20

FT /label= OTHER

FT /note= "C-terminal amide"

XX

PN US6221608-B1.

XX

PD 24-APR-2001.

XX

PF 22-JAN-1997; 97US-0786690.

XX

PR 22-JAN-1997; 97US-0786690.

XX

PA (ORTH) ORTHO PHARM CORP.

XX

PI Middleton SA, Johnson D, McMahon FJ, Mulkahy LS, Jolliffe LK;

XX WPI; 2001-327242/34.

XX

PT Identifying a modulator that dimerises a receptor, useful for

PT identifying and purifying erythropoietin receptor binding proteins -

XX

PS Example 10; Column 22; 30pp; English.

XX

CC The present invention describes a method of identifying a modulator that

CC dimerises a receptor, involving combining a test compound, a preformed

CC dimerisation template and a labeled receptor dimerising ligand, measuring

CC competitive binding of the test compound, adding the modulator to cells

CC which proliferate in response to ligand binding and measuring

CC proliferation of the cells in the presence of the test compound. In

CC particular, this is useful where the preformed dimerisation template is

CC an erythropoietin (EPO) receptor, such as EPO binding protein (EBP). This

CC method is useful in the drug discovery of proteins which bind to EBP.

XX

SQ Sequence 20 AA;

Query Match 95.1%; Score 117; DB 22; Length 20;

Best Local Similarity 95.0%; Pred. No. 3.1e-09;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWVCKPQGG 20

Db 1 GGTYSCHFGPLTWVCKPQGG 20

RESULT 23

AAB97492

ID AAB97492 standard; peptide; 20 AA.

XX

AC AAB97492;

XX

DT 03-AUG-2001 (first entry)

XX

DE Erythropoietin cyclic mimetic peptide #4.

XX

KW Erythropoietin; mimetic; EPO; cyclic; EPO binding protein; EBP;

KW drug discovery.

XX

OS Synthetic.

XX

PN US6221608-B1.

XX

PD 24-APR-2001.

XX

PF 22-JAN-1997; 97US-0786690.

XX

PR 22-JAN-1997; 97US-0786690.

XX

PA (ORTH) ORTHO PHARM CORP.

XX

PI Middleton SA, Johnson D, McMahon FJ, Mulkahy LS, Jolliffe LK;

XX

FT WPI; 2001-327242/34.

XX

PT Identifying a modulator that dimerises a receptor, useful for

PT identifying and purifying erythropoietin receptor binding proteins -

XX

PS Example 10; Column 31; 30pp; English.

XX

CC The present invention describes a method of identifying a modulator that

CC dimerises a receptor, involving combining a test compound, a preformed

CC dimerisation template and a labeled receptor dimerising ligand, measuring

CC competitive binding of the test compound, adding the modulator to cells

CC which proliferate in response to ligand binding and measuring

CC proliferation of the cells in the presence of the test compound. In

CC particular, this is useful where the preformed dimerisation template is

CC an erythropoietin (EPO) receptor, such as EPO binding protein (EBP). This

CC method is useful in the drug discovery of proteins which bind to EBP.

XX

CC Note: This sequence is stated in the specification as being the same as

CC that shown in column 22 of the specification. However, the sequences
CC differ at several positions.
XX
SQ Sequence 20 AA;

Query Match 95.1%; Score 117; DB 22; Length 20;
Best Local Similarity 95.0%; Pred. No. 3.le-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| ||||| ||||| |||||
Db 1 GGTYSCHFGLTWCKPQGG 20

RESULT 24
AAU74456
ID AAU74456 standard; Peptide; 20 AA.
XX
AC AAU74456;
XX
DT 09-APR-2002 (first entry)
XX
DE Human erythropoietin neuroprotective peptide EMP-1.
XX
KW Neuroprotective peptide; human; erythropoietin; neurotoxicity; anaemia;
KW erythropoietin receptor; EPO receptor; neurodegeneration; prion disease;
KW neurological damage; neurodegenerative disorder; neurological disorder;
KW psychiatric disorder; blood loss; renal failure; cancer; HIV; EMP-1;
KW human immunodeficiency virus; haematology; autoimmune disease;
KW inflammatory disorder; infectious disease.
XX
OS Homo sapiens.
XX
PN WO200191780-A1.
XX
PD 06-DEC-2001.
XX
PF 23-MAY-2001; 2001WO-US16654.
XX
PR 26-MAY-2000; 2000US-207654P.
XX
PA (ORTH) ORTHO-MCNEIL PHARM INC.
XX
PI Smith-Swintosky V, Renzi M, Plata-Salaman C, Jolliffe L, Farrell F;
PI Johnson DL;
XX
WPI; 2002-114307/15.
XX
PT Treating patients having condition mediated by neurotoxicity,
PT neurodegeneration or neurological damage, involves administering to
PT patient a peptide comprising monomeric peptides that bind to
PT erythropoietin receptor -
XX
PS Claim 14; Page 40; 75pp; English.
XX
CC The invention relates to a method for treating a patient with a condition
CC mediated by neurotoxicity, neurodegeneration or neurological damage,
CC involving administering a peptide comprising one or more monomeric
CC peptides that bind to the human erythropoietin (EPO) receptor. The method
CC is useful for treating acute and chronic neurodegenerative disorders
CC including cerebral ischaemia or infarction, Alzheimer's disease, Pick's
CC disease, diffuse Lewy body disease, Shy-Drager syndrome, amyotrophic
CC lateral sclerosis, Huntington's disease, Parkinson's disease, Gilles De
CC La Tourette's disease, Tay-Sach's disease, and prion diseases including
CC Creutzfeldt-Jakob and Kuru, neurological and psychiatric manifestations
CC associated with peripheral diseases including blood loss of any kind,
CC renal failure, conditions associated with anaemia, and neurological and
CC neuropsychiatric manifestations including haematological and
CC non-haematological malignancies/cancer, symptoms or complications in
CC patients receiving chemotherapy, inflammatory and infectious disorders
CC such as human immunodeficiency viral infections, and chronic systemic
CC autoimmune diseases such as systemic lupus erythematosus. The method is
CC also useful for prevention of plexopathies and neuropathies. This

CC sequence represents a human erythropoietin neuroprotective peptide of the
CC invention.
XX
SQ Sequence 20 AA;

Query Match 95.1%; Score 117; DB 23; Length 20;
Best Local Similarity 95.0%; Pred. No. 3.le-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| ||||| ||||| |||||
Db 1 GGTYSCHFGLTWCKPQGG 20

RESULT 25
AAU74478
ID AAU74478 standard; Peptide; 20 AA.
XX
AC AAU74478;
XX
DT 09-APR-2002 (first entry)
XX
DE Human erythropoietin neuroprotective peptide EMP-8.
XX
KW Neuroprotective peptide; human; erythropoietin; neurotoxicity; anaemia;
KW erythropoietin receptor; EPO receptor; neurodegeneration; prion disease;
KW neurological damage; neurodegenerative disorder; neurological disorder;
KW psychiatric disorder; blood loss; renal failure; cancer; HIV;
KW human immunodeficiency virus; haematology; autoimmune disease;
KW inflammatory disorder; infectious disease; EMP-8.
XX
OS Homo sapiens.
XX
PN WO200191780-A1.
XX
PD 06-DEC-2001.
XX
PF 23-MAY-2001; 2001WO-US16654.
XX
PR 26-MAY-2000; 2000US-207654P.
XX
PA (ORTH) ORTHO-MCNEIL PHARM INC.
XX
PI Smith-Swintosky V, Renzi M, Plata-Salaman C, Jolliffe L, Farrell F;
PI Johnson DL;
XX
WPI; 2002-114307/15.
XX
PT Treating patients having condition mediated by neurotoxicity,
PT neurodegeneration or neurological damage, involves administering to
PT patient a peptide comprising monomeric peptides that bind to
PT erythropoietin receptor -
XX
PS Claim 14; Page 41; 75pp; English.
XX
CC The invention relates to a method for treating a patient with a condition
CC mediated by neurotoxicity, neurodegeneration or neurological damage,
CC involving administering a peptide comprising one or more monomeric
CC peptides that bind to the human erythropoietin (EPO) receptor. The method
CC is useful for treating acute and chronic neurodegenerative disorders
CC including cerebral ischaemia or infarction, Alzheimer's disease, Pick's
CC disease, diffuse Lewy body disease, Shy-Drager syndrome, amyotrophic
CC lateral sclerosis, Huntington's disease, Parkinson's disease, Gilles De
CC La Tourette's disease, Tay-Sach's disease, and prion diseases including
CC Creutzfeldt-Jakob and Kuru, neurological and psychiatric manifestations
CC associated with peripheral diseases including blood loss of any kind,
CC renal failure, conditions associated with anaemia, and neurological and
CC neuropsychiatric manifestations including haematological and
CC non-haematological malignancies/cancer, symptoms or complications in
CC patients receiving chemotherapy, inflammatory and infectious disorders
CC such as human immunodeficiency viral infections, and chronic systemic
CC autoimmune diseases such as systemic lupus erythematosus. The method is
CC also useful for prevention of plexopathies and neuropathies. This

CC sequence represents a human erythropoietin neuroprotective peptide of the
CC invention.
XX
SQ Sequence 20 AA;
Query Match 95.1%; Score 117; DB 23; Length 20;
Best Local Similarity 95.0%; Pred. No. 3.1e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTFSCHFGPLTWCKPQGG 20
RESULT 26
AAU74486
ID AAU74486 standard; Peptide; 20 AA.
AC AAU74486;
XX
DT 09-APR-2002 (first entry)
DE Human erythropoietin neuroprotective peptide EMP-34.
XX
KW Neuroprotective peptide; human; erythropoietin; neurotoxicity; anaemia;
KW erythropoietin receptor; EPO receptor; neurodegeneration; prion disease;
KW neurological damage; neurodegenerative disorder; neurological disorder;
KW psychiatric disorder; blood loss; renal failure; cancer; HIV;
KW human immunodeficiency virus; haematology; autoimmune disease;
KW inflammatory disorder; infectious disease; EMP-34.
XX
OS Homo sapiens.
XX
FH Key location/Qualifiers
FT Modified-site 1
FT /note= "Acetyl-Glycine"
XX
FN WO200:9178C-A1.
XX
PD 06-DEC-2001.
XX
PF 23-MAY-2001; 2001WO-US16654.
XX
XX 26-MAY-2000; 2000US-2C7654P.
XX
PA (ORTH : ORTHO MCNEIL PHARM INC.
XX
FI Smith-Swintosky V, Renzi M, Piata-Salaman C, Colliffe L, Farrell F;
PI Johnson DL;
XX
DR WPI; 2002-114307/15.
XX
XX Treating patients having condition mediated by neurotoxicity,
PT neurodegeneration or neurological damage, involves administering to
PT patient a peptide comprising monomeric peptides that bind to
PT erythropoietin receptor -
XX
PS Claim 14; Page 41; 75pp; English.
XX
CC The invention relates to a method for treating a patient with a condition
CC mediated by neurotoxicity, neurodegeneration or neurological damage,
CC involving administering a peptide comprising one or more monomeric
CC peptides that bind to the human erythropoietin (EPO) receptor. The method
CC is useful for treating acute and chronic neurodegenerative disorders
CC including cerebral ischaemia or infarction, Alzheimer's disease, Pick's
CC disease, diffuse Lewy body disease, Shy-Drager syndrome, amyotrophic
CC lateral sclerosis, Huntington's disease, Parkinson's disease, Gilles De
CC La Tourette's disease, Tay-Sachs's disease, and prion diseases including
CC Creutzfeldt-Jakob and Kuru, neurological and psychiatric manifestations
CC associated with peripheral diseases including blood loss of any kind,
CC renal failure, conditions associated with anaemia, and neurological and
CC neuropsychiatric manifestations including haematological and
CC non-haematological malignancies/cancer, symptoms or complications in

CC patients receiving chemotherapy, inflammatory and infectious disorders
CC such as human immunodeficiency viral infections, and chronic systemic
CC autoimmune diseases such as systemic lupus erythematosus. The method is
CC also useful for prevention of plexopathies and neuropathies. This
CC sequence represents a human erythropoietin neuroprotective peptide of the
CC invention.
XX
SQ Sequence 20 AA;
Query Match 95.1%; Score 117; DB 23; Length 20;
Best Local Similarity 95.0%; Pred. No. 3.1e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTYSCHFGPLTWCKPQGG 20
RESULT 27
ABB72814
ID ABB72814 standard; Peptide; 20 AA.
XX
AC ABB72814;
XX
DT 05-APR-2002 (first entry)
DE Erythropoietin (EPO) mimetic peptide SEQ ID NO:87.
XX
KW Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG;
KW EPO; erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
KW TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP;
KW TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
KW MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
KW cytostatic; antirheumatic; antiarthritis; antidiabetic; ophthalmological;
KW antianaemic; anorectic; antiinfertility; haemostatic; dermatological;
KW neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
KW cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
KW sleep disorder; neurological degenerative disease; anaemia;
KW thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
KW Farconi's syndrome.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200183525-A2.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US14310.
XX
PR 03-MAY-2000; 2000US-0563286.
XX
XX (AMGE-) AMGEN INC.
PA
PI Feige U, Liu C, Cheetham JC, Boone TC, Gudas JM;
XX
DR WPI; 2002-130313/17.
XX
PT Novel vehicle-peptide molecule or its multimers useful for treating
PT inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
PT diabetic retinopathy, obesity, sleep disorders and infertility -
XX
PS Claim 39; Page 41; 176pp; English.
XX
CC The present invention describes a vehicle-peptide molecule (I) or its
CC multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
CC cytotstatic, antirheumatic, antiarthritis, antidiabetic, ophthalmological,
CC antianaemic, anorectic, antiinfertility, haemostatic, dermatological and
CC neuroprotective activities. (I) can be used as a therapeutic or
CC prophylactic agent as well as for screening purposes. (I) is useful for
CC diagnosing diseases characterised by dysfunction of their associated
CC protein of interest, for identifying normal or abnormal proteins of
CC interest, as a part of diagnostic kit to detect the presence of their

CC proteins of interest in a biological sample. Additionally, (I) is useful
CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,
CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
CC infertility, and neurological degenerative diseases. (I), comprising
CC EPO-mimetic compounds are useful for treating disorders characterised by
CC low red blood cell levels such as anaemia. The TPO-mimetic comprising
CC compounds are useful for treating conditions that involve an existing
CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
CC deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic
CC tumour which result in thrombocytopaenia, systemic lupus erythematosus,
CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777
CC represent amino acid and nucleic acid sequences used in the
CC exemplification of the present invention.

XX
SQ Sequence 20 AA;

Query Match 95.1%; Score 117; DB 23; Length 20;
Best Local Similarity 95.0%; Pred. No. 3.1e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
DB 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 28
ABB72840
ID ABB72840 standard; Peptide; 20 AA.
XX
AC ABB72840;
XX
DT 05-APR-2002 (first entry)
XX
DE Erythropoietin (EPO) mimetic peptide SEQ ID NO:1025.
XX
KW Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG;
KW EPO; erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
KW TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP;
KW TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
KW MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
KW cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
KW antianaemic; anorectic; antiinfertility; haemostatic; dermatological;
KW neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
KW cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
KW sleep disorder; neurological degenerative disease; anaemia;
KW thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
KW Fanconi's syndrome.

XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200183525-A2.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US14310.
XX
PR 03-MAY-2000; 2000US-0563286.
XX
PA (ANGE-) AMGEN INC.
XX
PI Feige U, Liu C, Cheetham JC, Boone TC, Gudas JM;
XX WPI; 2002-130313/17.
DR
XX
PT Novel vehicle-peptide molecule or its multimers useful for treating
PT inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
PT diabetic retinopathy, obesity, sleep disorders and infertility -
XX
PS Claim 39; Page 42; 176pp; English.
XX
CC The present invention describes a vehicle-peptide molecule (I) or its
CC multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,

CC cytotstatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,
CC antianaemic, anorectic, antiinfertility, haemostatic, dermatological and
CC neuroprotective activities. (I) can be used as a therapeutic or
CC prophylactic agent as well as for screening purposes. (I) is useful for
CC diagnosing diseases characterised by dysfunction of their associated
CC protein of interest, for identifying normal or abnormal proteins of
CC interest, as a part of diagnostic kit to detect the presence of their
CC proteins of interest in a biological sample. Additionally, (I) is useful
CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,
CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
CC infertility, and neurological degenerative diseases. (I), comprising
CC EPO-mimetic compounds are useful for treating disorders characterised by
CC low red blood cell levels such as anaemia. The TPO-mimetic comprising
CC compounds are useful for treating conditions that involve an existing
CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
CC deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic
CC tumour which result in thrombocytopaenia, systemic lupus erythematosus,
CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777
CC represent amino acid and nucleic acid sequences used in the
CC exemplification of the present invention.

XX
SQ Sequence 20 AA;

Query Match 95.1%; Score 117; DB 23; Length 20;
Best Local Similarity 95.0%; Pred. No. 3.1e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
DB 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 29
ABB57650
ID ABB57650 standard; Peptide; 20 AA.
XX
AC ABB57650;
XX
DT 18-MAR-2002 (first entry)
XX
DE Erythropoietin receptor peptide agonist.
XX
KW Antirheumatic; antiarthritic; osteopathic; cartilage disorder;
KW insulin-like growth factor; IGF; binding protein; IGFBP;
KW rheumatoid arthritis; osteoarthritis; erythropoietin; agonist.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 6..15
XX
PN WO200187323-A2.
XX
PD 22-NOV-2001.
XX
PF 16-MAY-2001; 2001WO-US15904.
XX
PR 16-MAY-2000; 2000US-204490P.
PR 15-NOV-2000; 2000US-248985P.
XX
PA (GETH) GENENTECH INC.
XX
PI Dubaquitte Y, Filvaroff EH, Lowman HB;
XX WPI; 2002-082942/11.
DR
XX
PT Treating cartilage disorders including cartilage damage by injury or
PT degenerative cartilaginous disorders, by contacting cartilage with
PT insulin-like growth factor analog with altered affinity for IGF-binding
PT proteins -
XX
PS Example 1; Page 40; 136pp; English.
XX

CC The present invention relates to a method for treating cartilage disorders. The method comprises contacting cartilage with an active agent such as insulin-like growth factor (IGF-1) analog with a binding affinity preference for IGF binding protein-3 (IGFBP-3) over IGFBP-1, an IGF-1 analog with a binding affinity preference for IGFBP-1 over IGFBP-3, or a IGFBP displacer peptide that prevents the interaction of IGF with an IGFBP and does not bind to human IGF receptor. The method is useful for treating cartilage disorders (CD), including degenerative CD, articular CD such as rheumatoid arthritis and osteoarthritis. The present sequence was used to illustrate the invention.

XX Sequence 20 AA;
SQ Query Match 95.1%; Score 117; DB 23; Length 20;
Best Local Similarity 95.0%; Pred. No. 3.1e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 30
AAY13638
ID AAY13638 standard; peptide; 22 AA.

XX AC AAY13638;
XX DT 06-SEP-1999 (first entry)
XX DE Erythropoietin receptor (EPO-R) binding peptide.
XX KW Erythropoietin; EPO; receptor; EPO deficiency; renal failure; AIDS; dialysis; anaemia; autoimmune disease; chronic inflammatory disease; malignancy; beta-thalassaemia; cystic fibrosis; prematurity; blood loss; spinal cord injury; aging; neoplastic disease; erythropoiesis; EPO-R.

XX OS Synthetic.
XX PN WC9643749-A1.
XX PD 19-DEC-1996.
XX PF 07-JUN-1996; 96WO-US09810.

XX PR 07-JUN-1995; 95US-0484635.
XX PR 07-JUN-1995; 95US-0484631.
XX PR 19-NOV-1993; 93US-0155940.

XX PA (AFFY-) AFFYMAX TECHNOLOGIES NV.
XX PA (COHJ) JOHNSON & JOHNSON CORP.
XX PA (ORTH) ORTHO PHARM CORP.

XX PI Chang RS, Dower WJ, Johnson D, Jolliffe LK, Kashyap AK;
XX PI Mulcahy L, Wrighton NC;
XX DR WPI; 1997-052225/05.

XX PT Erythropoietin receptor binding peptide - useful for treating disorders characterised by deficiency of EPO, or low or defective red blood cell population
XX PS Claim 6; Page 68; 95pp; English.

XX CC The invention describes a peptide of 10-40 amino acid residues which binds to erythropoietin (EPO) receptor and which includes the amino acid sequence Cys-Xaa1-Xaa2-Gly-Pro-Xaa3-Thr-Trp-Xaa4-Cys, where Xaa1 = Arg, His, Leu or Trp, Xaa2 = Met, Phe or Ile, Xaa3 = 1 of the 20 genetically coded L-amino acids, and Xaa4 = Asp, Glu, Ile, Leu or Val. Optionally, the peptide may be cyclised or dimerised. The peptide can be used to treat a patient having a disorder characterised by a deficiency of EPO or a low or defective red blood cell population. It can be used to treat end stage renal failure or dialysis; anaemia associated with AIDS,

CC autoimmune disease, chronic inflammatory diseases or malignancy;
CC beta-thalassaemia; cystic fibrosis; early anaemia of prematurity; spinal cord injury; acute blood loss; aging; and neoplastic disease states accompanied by abnormal erythropoiesis. The peptides can also be used as reagents for detecting EPO receptors on living cells, in biological fluids, in tissue homogenates, etc. Sequences AAY13624-661 represent specific examples of EPO-R binding peptides.

XX SQ Sequence 22 AA;
SQ Query Match 95.1%; Score 117; DB 18; Length 22;
Best Local Similarity 95.0%; Pred. No. 3.4e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
Db 3 GGTYSCHFGPLTWCKPQGG 22

RESULT 31
AAB17041
ID AAB17041 standard; Peptide; 22 AA.

XX AC AAB17041;
XX DT 31-OCT-2000 (first entry)
XX DE EPO-mimetic peptide sequence SEQ ID NO:97.
XX KW Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.

XX OS Synthetic.
XX PN WO200024782-A2.
XX PD 04-MAY-2000.
XX PF 25-OCT-1999; 99WO-US25044.

XX PR 23-OCT-1998; 98US-0105371.
XX PR 22-OCT-1999; 99US-0428082.
XX PA (AMGE-) AMGEN INC.

XX PI Feige U, Liu C, Cheetham J, Boone TC;
XX DR WPI; 2000-350702/30.

XX PT Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and autoimmune diseases -
XX PS Claim 13; Page 229; 608pp; English.

XX CC The present invention describes composition of matter (I) comprising an Fc domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently 0 or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases.

CC The use of an Fc domain (rather than a Fab domain) can provide a longer
CC half-life or incorporate functions such as Fc receptor binding, protein
CC A binding, complement fixation, and possibly placental transfer. AAA69443
CC to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid
CC sequences used in the exemplification of the present invention.

XX
SQ Sequence 22 AA;
Query Match 95.1%; Score 117; DB 21; Length 22;
Best Local Similarity 95.0%; Pred. No. 3.4e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| ||||| ||||| |||||
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 32
ABB72824
ID ABB72824 standard; Peptide; 22 AA.

AC ABB72824;

XX
DT 05-APR-2002 (first entry)

DE Erythropoietin (EPO) mimetic peptide SEQ ID NO:97.

XX
KW Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG;
KW EPO; erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
KW TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP;
KW TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
KW MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
KW cytostatic; antirheumatic; antiarthritis; antidiabetic; ophthalmological;
KW artianaemic; anorectic; antiinfectivity; haemostatic; dermatological;
KW neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
KW cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
KW sleep disorder; neurological degenerative disease; anaemia;
KW thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
KW Fanconi's syndrome.

XX Homo sapiens.

OS Synthetic.

XX WO200183525-A2.

PN 08-NOV-2001.

XX 02-MAY-2001; 2001WO-US14310.

PF 03-MAY-2000; 2000US-0563286.

XX (AMGE-) AMGEN INC.

PA Feige U, Liu C, Cheetham JC, Boone TC, Gudas JM;

XX WPI; 2002-130313/17.

DR Novel vehicle-peptide molecule or its multimers useful for treating
XX inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
PT diabetic retinopathy, obesity, sleep disorders and infertility -
XX
PS Claim 39; Page 41; 176pp; English.

XX The present invention describes a vehicle-peptide molecule (I) or its
CC multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
CC cytostatic, antirheumatic, antiarthritis, antidiabetic, ophthalmological,
CC antianaemic, anorectic, antiinfertility, haemostatic, dermatological and
CC neuroprotective activities. (I) can be used as a therapeutic or
CC prophylactic agent as well as for screening purposes. (I) is useful for
CC diagnosing diseases characterised by dysfunction of their associated
CC proteins of interest, for identifying normal or abnormal proteins of
CC interest, as a part of diagnostic kit to detect the presence of their
CC proteins of interest in a biological sample. Additionally, (I) is useful

CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,
CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
CC infertility, and neurological degenerative diseases. (I), comprising
CC EPO-mimetic compounds are useful for treating disorders characterised by
CC low red blood cell levels such as anaemia. The TPO-mimetic comprising
CC compounds are useful for treating conditions that involve an existing
CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
CC deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic
CC tumour which result in thrombocytopaenia, systemic lupus erythematosus,
CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777
CC represent amino acid and nucleic acid sequences used in the
CC exemplification of the present invention.

XX Sequence 22 AA;

Query Match 95.1%; Score 117; DB 23; Length 22;
Best Local Similarity 95.0%; Pred. No. 3.4e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| ||||| ||||| |||||
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 33

AAAY26551

ID AAY26551 standard; peptide; 23 AA.

XX AAY26551;

AC AAY26551;

XX 06-SEP-1999 (first entry)

DT Erythropoietin receptor (EPO-R) binding peptide.

XX Erythropoietin; EPO; receptor; EPO deficiency; renal failure; AIDS;
OS dialysis; anaemia; autoimmune disease; chronic inflammatory disease;
XX malignancy; beta-thalassaemia; cystic fibrosis; prematurity; blood loss;
XX spinal cord injury; aging; neoplastic disease; erythropoiesis; EPO-R.

XX Synthetic.

XX WO9640749-A1.

XX 19-DEC-1996.

PD 07-JUN-1996; 96WO-US09810.

XX 07-JUN-1995; 95US-0484635.

XX 07-JUN-1995; 95US-0484631.

XX 19-NOV-1993; 93US-0155940.

XX (AFFY-) AFFYMAX TECHNOLOGIES NV.

PA (JOHJ) JOHNSON & JOHNSON CORP.

PA (ORTH) ORTHO PHARM CORP.

XX Chang RS, Dower WJ, Johnson D, Jolliffe LK, Kashyap AK;

PI Mulcahy L, Wrighton NC;

XX WPI; 1997-052225/05.

DR Erythropoietin receptor binding peptide - useful for treating
XX disorders characterised by deficiency of EPO, or low or defective
XX red blood cell population
PS Disclosure; Page 28; 95pp; English.

XX The invention describes a peptide of 10-40 amino acid residues which
CC binds to erythropoietin (EPO) receptor and which includes the amino acid
CC sequence Cys-Xaa1-Xaa2-Gly-Pro-Xaa3-Thr-Tip-Xaa4-Cys, where Xaa1 = Arg,
CC His, Leu or Trp, Xaa2 = Met, Phe or Ile, Xaa3 = 1 of the 20 genetically
CC coded L-amino acids, and Xaa4 = Asp, Glu, Ile, Leu or Val. Optionally,
CC the peptide may be cyclised or dimerised. The peptide can be used to
CC treat a patient having a disorder characterised by a deficiency of EPO

CC or a low or defective red blood cell population. It can be used to treat
CC end stage renal failure or dialysis; anaemia associated with AIDS;
CC autoimmune disease, chronic inflammatory diseases or malignancy;
CC beta-thalassaemia; cystic fibrosis; early anaemia of prematurity; spinal
CC cord injury; acute blood loss; aging; and neoplastic disease states
CC accompanied by abnormal erythropoiesis. The peptides can also be used as
CC reagents for detecting EPO receptors on living cells, in biological
CC fluids, in tissue homogenates, etc. Sequences AAY26352-548 are
CC representative peptides falling within the above peptide motif and
CC isolated during the affinity selection process.

SQ Sequence 23 AA;
Query Match 95.1%; Score 117; DB 18; Length 23;
Best Local Similarity 95.0%; Pred. No. 3.5e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY : GGTASCHFGPLTWCKPQGG 20
||| ||||| ||||| |||||
Db : GGTYSCHFGPLTWCKPQGG 20

RESULT 34
AAB17038
ID AAB17038 standard; Peptide; 23 AA.

XX AAB17038;
AC
XX 31-OCT-2000 (first entry)
XX
DE EPO-mimetic peptide sequence SEQ ID NO:94.
XX Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist;
KW MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
KW vascular endothelial growth factor; matrix metalloproteinase;
KW asthma; thrombosis; pharmaceutical.

XX Synthetic.
XX WO200024782-A2.
XX 04-MAY-2000.
XX 25-OCT-1999; 99WO-US25044.
XX 23-OCT-1998; 98US-0105371.
XX 22-OCT-1999; 99US-0428082.
XX (AMGE-) AMGEN INC.
XX Feige U, Liu C, Cheetham J, Boone TC;
XX WPI; 2000-350702/30.
XX Novel composition of matter comprising an Fc domain and
PT pharmacologically active peptides, useful for treating cancer and
PT autoimmune diseases -

XX Claim 13; Page 227; 608pp; English.
XX The present invention describes composition of matter (I) comprising an
CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2,
CC -(L1)c-P1-(L2)d-P2-(L3)e-P³, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
CC where P1, P2, P3, and P4 = are each independently sequences of
CC pharmacologically active peptides; L1, L2, L3, and L4 = are each
CC independently linkers; and a, b, c, d, e, and f = are each independently
CC 0 or 1, provided that at least 1 of a and b is 1. The composition can
CC have cytostatic, antiasthmatic, thrombolytic and immunosuppressive

CC activities. DNAs, vectors and host cells from the present invention can
CC be used for producing pharmaceutical compositions. The compositions are
CC useful for treating cancer, asthma, thrombosis, or autoimmune diseases.
CC The use of an Fc domain (rather than a Fab domain) can provide a longer
CC half-life or incorporate functions such as Fc receptor binding, protein
CC A binding, complement fixation, and possibly placental transfer. AAA69443
CC to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid
CC sequences used in the exemplification of the present invention.

SQ Sequence 23 AA;
Query Match 95.1%; Score 117; DB 21; Length 23;
Best Local Similarity 95.0%; Pred. No. 3.5e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY : 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| ||||| |||||
Db : 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 35
AAB17042
ID AAB17042 standard; Peptide; 23 AA.

XX AAB17042;
AC
XX 31-OCT-2000 (first entry)
XX
DE EPO-mimetic peptide sequence SEQ ID NO:98.
XX Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist;
KW MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
KW vascular endothelial growth factor; matrix metalloproteinase;
KW asthma; thrombosis; pharmaceutical.

XX Synthetic.
XX WO200024782-A2.
XX 04-MAY-2000.
XX 25-OCT-1999; 99WO-US25044.
XX 23-OCT-1998; 98US-0105371.
XX 22-OCT-1999; 99US-0428082.
XX (AMGE-) AMGEN INC.
XX Feige U, Liu C, Cheetham J, Boone TC;
XX WPI; 2000-350702/30.
XX Novel composition of matter comprising an Fc domain and
PT pharmacologically active peptides, useful for treating cancer and
PT autoimmune diseases -

XX Claim 13; Page 229; 608pp; English.
XX The present invention describes composition of matter (I) comprising an
CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2,
CC -(L1)c-P1-(L2)d-P2-(L3)e-P³, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
CC where P1, P2, P3, and P4 = are each independently sequences of
CC pharmacologically active peptides; L1, L2, L3, and L4 = are each
CC independently linkers; and a, b, c, d, e, and f = are each independently
CC 0 or 1, provided that at least 1 of a and b is 1. The composition can
CC have cytostatic, antiasthmatic, thrombolytic and immunosuppressive
CC activities. DNAs, vectors and host cells from the present invention can
CC be used for producing pharmaceutical compositions. The compositions are

CC useful for treating cancer, asthma, thrombosis, or autoimmune diseases.
 CC The use of an Fc domain (rather than a Fab domain) can provide a longer
 CC half-life or incorporate functions such as Fc receptor binding, protein
 CC A binding, complement fixation, and possibly placental transfer. AAA69443
 CC to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid
 CC sequences used in the exemplification of the present invention.
 XX
 SQ Sequence 23 AA;

Query Match 95.1%; Score 117; DB 21; Length 23;
 Best Local Similarity 95.0%; Pred. No. 3.5e-09;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
 ||| |||||
 Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 36
 ABB72821
 ID ABB72821 standard; Peptide; 23 AA.

XX AC ABB72821;

XX DT 05-APR-2002 (first entry)

XX DE Erythropoietin (EPO) mimetic peptide SEQ ID NO:94.

XX KW Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG;
 KW EPO; erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
 KW TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP;
 KW TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
 KW MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
 KW cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
 KW antianaemic; anorectic; antiinfertility; haemostatic; dermatological;
 KW neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
 KW cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
 KW sleep disorder; neurological degenerative disease; anaemia;
 KW thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
 KW Fanconi's syndrome.

XX OS Homo sapiens.
 OS Synthetic.

XX X: WO200183525-A2.

XX PD 08-NOV-2001.

XX PF 02-MAY-2001; 2001WO-US14310.

XX PR 03-MAY-2000; 2000US-0563286.

XX PA (AMGE-) AMGEN INC.

XX PI Feige U, Liu C, Cheetham JC, Boone TC, Gudas JM;

XX DR WPI; 2002-130313/17.

XX PT Novel vehicle-peptide molecule or its multimers useful for treating
 PT inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
 PT diabetic retinopathy, obesity, sleep disorders and infertility -

XX PS Claim 39; Page 41; 176pp; English.

XX CC The present invention describes a vehicle-peptide molecule (I) or its
 CC multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
 CC cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,
 CC antianaemic, anorectic, antiinfertility, haemostatic, dermatological and
 CC neuroprotective activities. (I) can be used as a therapeutic or
 CC prophylactic agent as well as for screening purposes. (I) is useful for
 CC diagnosing diseases characterised by dysfunction of their associated
 CC protein of interest, for identifying normal or abnormal proteins of
 CC interest, as a part of diagnostic kit to detect the presence of their

CC proteins of interest in a biological sample. Additionally, (I) is useful
 CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,
 CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
 CC infertility, and neurological degenerative diseases. (I), comprising
 CC EPO-mimetic compounds are useful for treating disorders characterised by
 CC low red blood cell levels such as anaemia. The TPO-mimetic comprising
 CC compounds are useful for treating conditions that involve an existing
 CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
 CC deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic
 CC tumour which result in thrombocytopaenia, systemic lupus erythematosus,
 CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777
 CC represent amino acid and nucleic acid sequences used in the
 CC exemplification of the present invention.

XX SQ Sequence 23 AA;

Query Match 95.1%; Score 117; DB 23; Length 23;
 Best Local Similarity 95.0%; Pred. No. 3.5e-09;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
 ||| |||||
 Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 37

ABB72825

ID ABB72825 standard; Peptide; 24 AA.

XX AC ABB72825;

XX DT 05-APR-2002 (first entry)

XX DE Erythropoietin (EPO) mimetic peptide SEQ ID NO:98.

XX KW Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG;
 KW EPO; erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
 KW TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP;
 KW TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
 KW MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
 KW cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
 KW antianaemic; anorectic; antiinfertility; haemostatic; dermatological;
 KW neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
 KW cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
 KW sleep disorder; neurological degenerative disease; anaemia;
 KW thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
 KW Fanconi's syndrome.

XX OS Homo sapiens.
 OS Synthetic.

XX PN WO200183525-A2.

XX PD 08-NOV-2001.

XX PF 02-MAY-2001; 2001WO-US14310.

XX PR 03-MAY-2000; 2000US-0563286.

XX PA (AMGE-) AMGEN INC.

XX PI Feige U, Liu C, Cheetham JC, Boone TC, Gudas JM;

XX DR WPI; 2002-130313/17.

XX PT Novel vehicle-peptide molecule or its multimers useful for treating
 PT inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
 PT diabetic retinopathy, obesity, sleep disorders and infertility -

XX PS Claim 39; Page 41; 176pp; English.

XX CC The present invention describes a vehicle-peptide molecule (I) or its
 CC multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,

CC cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,
CC antianaemic, anorectic, antiinflammatory, haemostatic, dermatological and
CC neuroprotective activities. (I) can be used as a therapeutic or
CC prophylactic agent as well as for screening purposes. (I) is useful for
CC diagnosing diseases characterised by dysfunction of their associated
CC protein of interest, for identifying normal or abnormal proteins of
CC interest, as a part of diagnostic kit to detect the presence of their
CC proteins of interest in a biological sample. Additionally, (I) is useful
CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,
CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
CC infertility, and neurological degenerative diseases. (I), comprising
CC EPO-mimetic compounds are useful for treating disorders characterised by
CC low red blood cell levels such as anaemia. The TPO-mimetic comprising
CC compounds are useful for treating conditions that involve an existing
CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
CC deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic
CC tumour which result in thrombocytopaenia, systemic lupus erythematosus,
CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777
CC represent amino acid and nucleic acid sequences used in the
CC exemplification of the present invention.

XX
SQ Sequence 24 AA;
Query Match 95.1%; Score 117; DB 23; Length 24;
Best Local Similarity 95.0%; Pred. No. 3.7e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| ||||| ||||| |||||
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 38
ABB73394
ID ABB73394 standard; Peptide; 25 AA.

XX ABB73394;

DT 05-APR-2002 (first entry)

DE EPO-mimetic peptide SEQ ID NO:1034.

XX Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG;
KW EPC; erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
KW TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP;
KW TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
KW MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
KW cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
KW antianaemic; anorectic; antiinfertility; haemostatic; dermatological;
KW neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
KW cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
KW sleep disorder; neurological degenerative disease; anaemia;
KW thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
KW Fanconi's syndrome.

XX Homo sapiens.

OS Synthetic.

XX WO200183525-A2.

PN 08-NOV-2001.

XX 02-MAY-2001; 2001WO-US14310.

PF 03-MAY-2000; 2000US-0563286.

XX (AMGE-) AMGEN INC.

XX Feige U, Liu C, Cheetham JC, Boone TC, Gudas JM;

PI WPI; 2002-130313/17.

DR Novel vehicle-peptide molecule or its multimers useful for treating

PT inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
PT diabetic retinopathy, obesity, sleep disorders and infertility -
XX Disclosure; Page 90; 176pp; English.
PS The present invention describes a vehicle-peptide molecule (I) or its
XX multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
CC cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,
CC antianaemic, anorectic, antiinfertility, haemostatic, dermatological and
CC neuroprotective activities. (I) can be used as a therapeutic or
CC prophylactic agent as well as for screening purposes. (I) is useful for
CC diagnosing diseases characterised by dysfunction of their associated
CC protein of interest, for identifying normal or abnormal proteins of
CC interest, as a part of diagnostic kit to detect the presence of their
CC proteins of interest in a biological sample. Additionally, (I) is useful
CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,
CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
CC infertility, and neurological degenerative diseases. (I), comprising
CC EPO-mimetic compounds are useful for treating disorders characterised by
CC low red blood cell levels such as anaemia. The TPO-mimetic comprising
CC compounds are useful for treating conditions that involve an existing
CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
CC deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic
CC tumour which result in thrombocytopaenia, systemic lupus erythematosus,
CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777
CC represent amino acid and nucleic acid sequences used in the
CC exemplification of the present invention.

XX Sequence 25 AA;

Query Match 95.1%; Score 117; DB 23; Length 25;

Best Local Similarity 95.0%; Pred. No. 3.8e-09;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| ||||| ||||| |||||
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 39

AAB17930

ID AAB17930 standard; Peptide; 26 AA.

XX AAB17930;

XX 31-OCT-2000 (first entry)

DE EPO-mimetic peptide sequence SEQ ID NO:1034.

XX Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist;
KW MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
KW vascular endothelial growth factor; matrix metalloproteinase;
KW asthma; thrombosis; pharmaceutical.

OS Synthetic.

XX WO2000024782-A2.

PN 04-MAY-2000.

XX 25-OCT-1999; 99WO-US25044.

XX 23-OCT-1998; 98US-0105371.

XX 22-OCT-1999; 99US-0428082.

XX (AMGE-) AMGEN INC.

PI Feige U, Liu C, Cheetham J, Boone TC;

XX WPI; 2000-350702/30.

XX Novel composition of matter comprising an Fc domain and
PT pharmacologically active peptides, useful for treating cancer and
PT autoimmune diseases -

PS Disclosure; Page 559; 608pp; English.

XX The present invention describes composition of matter (I) comprising an
CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2,
CC -(L1)c-P1-(L2)d-P2-(L3)e-P³, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
CC where P1, P2, P3, and P4 = are each independently sequences of
CC pharmacologically active peptides; L1, L2, L3, and L4 = are each
CC independently linkers; and a, b, c, d, e, and f = are each independently
CC 0 or 1, provided that at least 1 of a and b is 1. The composition can
CC have cytostatic, antiasthmatic, thrombolytic and immunosuppressive
CC activities. DNAs, vectors and host cells from the present invention can
CC be used for producing pharmaceutical compositions. The compositions are
CC useful for treating cancer, asthma, thrombosis, or autoimmune diseases.
CC The use of an Fc domain (rather than a Fab domain) can provide a longer
CC half-life or incorporate functions such as Fc receptor binding, protein
CC A binding, complement fixation, and possibly placental transfer. AAA69443
CC to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid
CC sequences used in the exemplification of the present invention.

XX Sequence 26 AA;

Query Match 95.1%; Score 117; DB 21; Length 26;
Best Local Similarity 95.0%; Pred. No. 4e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| ||||| ||||| |||||
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 40

AAB17313
ID AAB17313 standard; Peptide; 36 AA.

XX AAB17313;

DT 31-OCT-2000 (first entry)

XX EMP-Fc fusion construction peptide SEQ ID NO:403.

DE Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist;
KW MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
KW vascular endothelial growth factor; matrix metalloproteinase;
KW asthma; thrombosis; pharmaceutical.

XX Homo sapiens.
OS Synthetic.

XX WO200024782-A2.

XX 04-MAY-2000.

XX 25-OCT-1999; 99WO-US25044.

XX 23-OCT-1998; 98US-0105371.

PR 22-OCT-1999; 99US-0428082.

XX (AMGE-) AMGEN INC.

XX Feige U, Liu C, Cheetham J, Boone TC;

XX WPI; 2000-350702/30.

XX

PT Novel composition of matter comprising an Fc domain and
PT pharmacologically active peptides, useful for treating cancer and
PT autoimmune diseases -

XX Example 3; Page 337; 608pp; English.

XX The present invention describes composition of matter (I) comprising an
CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2,
CC -(L1)c-P1-(L2)d-P2-(L3)e-P³, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
CC where P1, P2, P3, and P4 = are each independently sequences of
CC pharmacologically active peptides; L1, L2, L3, and L4 = are each
CC independently linkers; and a, b, c, d, e, and f = are each independently
CC 0 or 1, provided that at least 1 of a and b is 1. The composition can
CC have cytostatic, antiasthmatic, thrombolytic and immunosuppressive
CC activities. DNAs, vectors and host cells from the present invention can
CC be used for producing pharmaceutical compositions. The compositions are
CC useful for treating cancer, asthma, thrombosis, or autoimmune diseases.
CC The use of an Fc domain (rather than a Fab domain) can provide a longer
CC half-life or incorporate functions such as Fc receptor binding, protein
CC A binding, complement fixation, and possibly placental transfer. AAA69443
CC to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid
CC sequences used in the exemplification of the present invention.

XX Sequence 36 AA;

Query Match 95.1%; Score 117; DB 21; Length 36;
Best Local Similarity 95.0%; Pred. No. 5.4e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| ||||| ||||| |||||
Db 12 GGTYSCHFGPLTWCKPQGG 31

RESULT 41

ABB73407
ID ABB73407 standard; Peptide; 36 AA.

XX ABB73407;

XX 05-APR-2002 (first entry)

XX EPO mimetic peptide gene construction related peptide SEQ ID NO:403.

DE Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG;
KW EPO; erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
KW TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP;
KW TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
KW MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
KW cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
KW antianaemic; anorectic; antiinfertility; haemostatic; dermatological;
KW neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
KW cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
KW sleep disorder; neurological degenerative disease; anaemia;
KW thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
KW Fanconi's syndrome.

XX Homo sapiens.
OS Synthetic.

XX WO200183525-A2.

XX 08-NOV-2001.

XX 02-MAY-2001; 2001WO-US14310.

XX 03-MAY-2000; 2000US-0563286.

XX (AMGE-) AMGEN INC.

XX Feige U, Liu C, Cheetham JC, Boone TC, Gudas JM;

XX WPI; 2002-130313/17.
XX Novel vehicle-peptide molecule or its multimers useful for treating
PT inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
PT diabetic retinopathy, obesity, sleep disorders and infertility.
XX Example 3; Page 114; 176pp; English.
PS The present invention describes a vehicle-peptide molecule (I) or its
XX multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
CC cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,
CC antianaemic, anorectic, antiinfertility, haemostatic, dermatological and
CC neuroprotective activities. (I) can be used as a therapeutic or
CC prophylactic agent as well as for screening purposes. (I) is useful for
CC diagnosing diseases characterised by dysfunction of their associated
CC protein of interest, for identifying normal or abnormal proteins of
CC interest, as a part of diagnostic kit to detect the presence of their
CC proteins of interest in a biological sample. Additionally, (I) is useful
CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,
CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
CC infertility, and neurological degenerative diseases. (I), comprising
CC EPO-mimetic compounds are useful for treating disorders characterised by
CC low red blood cell levels such as anaemia. The TPO-mimetic comprising
CC compounds are useful for treating conditions that involve an existing
CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
CC deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic
CC tumour which result in thrombocytopaenia, systemic lupus erythematosus,
CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777
CC represent amino acid and nucleic acid sequences used in the
CC exemplification of the present invention.
XX
SQ Sequence 36 AA;

Query Match 95.1%; Score 117; DB 23; Length 36;
Best Local Similarity 95.0%; Pred. No. 5.4e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
Db 12 GGTYSCHFGPLTWCKPQGG 31

RESULT 42
AAB17312
ID AAB17312 standard; Peptide; 39 AA.
XX
AC AAB17312;

DT 31-OCT-2000 (first entry)
XX
DE FC-EMP fusion construction peptide SEQ ID NO:395.

XX Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist;
KW MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
KW vascular endothelial growth factor; matrix metalloproteinase;
KW asthma; thrombosis; pharmaceutical.

XX Homo sapiens.
OS Synthetic.
XX WO200024782-A2.
XX
XX 04-MAY-2000.
XX
XX 25-OCT-1999; 99WO-US25044.
XX
XX 23-OCT-1998; 98US-0105371.
XX 22-OCT-1999; 99US-0428082.

PA (AMGE-) AMGEN INC.
XX
PI Feige U, Liu C, Cheetham J, Boone TC;
XX WPI; 2000-350702/30.
XX
PT Novel composition of matter comprising an Fc domain and
PT pharmacologically active peptides, useful for treating cancer and
PT autoimmune diseases.
XX
XX Example 3; Page 335; 608pp; English.
PS The present invention describes composition of matter (I) comprising an
XX Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2,
CC -(L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
CC where P1, P2, P3, and P4 = are each independently sequences of
CC pharmacologically active peptides; L1, L2, L3, and L4 = are each
CC independently linkers; and a, b, c, d, e, and f = are each independently
CC 0 or 1, provided that at least 1 of a and b is 1. The composition can
CC have cytostatic, antiasthmatic, thrombolytic and immunosuppressive
CC activities. DNAs, vectors and host cells from the present invention can
CC be used for producing pharmaceutical compositions. The compositions are
CC useful for treating cancer, asthma, thrombosis, or autoimmune diseases.
CC The use of an Fc domain (rather than a Fab domain) can provide a longer
CC half-life or incorporate functions such as Fc receptor binding, protein
CC A binding, complement fixation, and possibly placental transfer. AAA69443
CC to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid
CC sequences used in the exemplification of the present invention.
XX
SQ Sequence 39 AA;

Query Match 95.1%; Score 117; DB 21; Length 39;
Best Local Similarity 95.0%; Pred. No. 5.8e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
Db 8 GGTYSCHFGPLTWCKPQGG 27

RESULT 43
ABB73406
ID ABB73406 standard; Peptide; 39 AA.

XX ABB73406;
XX
DT 05-APR-2002 (first entry)
XX
DE EPO mimetic peptide gene construction related peptide SEQ ID NO:395.
XX
KW Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG;
KW EPO; erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
KW TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP;
KW TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
KW MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
KW cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
KW antianaemic; anorectic; antiinfertility; haemostatic; dermatological;
KW neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
KW cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
KW sleep disorder; neurological degenerative disease; anaemia;
KW thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
KW Fanconi's syndrome.

XX Homo sapiens.
OS Synthetic.
XX WO200183525-A2.
XX
XX 08-NOV-2001.
XX
XX 02-MAY-2001; 2001WO-US14310.

XX 03-MAY-2000; 2000US-0563286.
PR (AMGE-) AMGEN INC.
PA Feige U, Liu C, Cheetham JC, Boone TC, Gudas JM;
PI WPI; 2002-130313/17.
XX
DR Novel vehicle-peptide molecule or its multimers useful for treating
XX inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
PT diabetic retinopathy, obesity, sleep disorders and infertility -
XX
PS Example 3; Page 112; 176pp; English.
XX
CC The present invention describes a vehicle-peptide molecule (I) or its
CC multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
CC cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,
CC antianaemic, anorectic, antiinfertility, haemostatic, dermatological and
CC neuroprotective activities. (I) can be used as a therapeutic or
CC prophylactic agent as well as for screening purposes. (I) is useful for
CC diagnosing diseases characterised by dysfunction of their associated
CC protein of interest, for identifying normal or abnormal proteins of
CC interest, as a part of diagnostic kit to detect the presence of their
CC proteins of interest in a biological sample. Additionally, (I) is useful
CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,
CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
CC infertility, and neurological degenerative diseases. (I), comprising
CC EPO-mimetic compounds are useful for treating disorders characterised by
CC low red blood cell levels such as anaemia. The TPO-mimetic comprising
CC compounds are useful for treating conditions that involve an existing
CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
CC deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic
CC tumour which result in thrombocytopaenia, systemic lupus erythematosus,
CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777
CC represent amino acid and nucleic acid sequences used in the
CC exemplification of the present invention.
XX
SQ Sequence 39 AA;
Query Match 95.1%; Score 117; DB 23; Length 39;
Best Local Similarity 95.0%; Pred. No. 5.8e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGTASCHFGPLTWCKPQGG 20
Db 8 GGTYSCHFGPLTWCKPQGG 27
RESULT 44
AAB17036
ID AAB17036 standard; Peptide; 40 AA.
XX
AC AAB17036;
XX
DT 31-OCT-2000 (first entry)
XX
DE EPO-mimetic peptide sequence SEQ ID NO:92.
XX
KW Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist;
KW MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
KW vascular endothelial growth factor; matrix metalloproteinase;
KW asthma; thrombosis; pharmaceutical.
XX
OS Synthetic.
XX
PN WO200024782-A2.
XX
PD 04-MAY-2000.
XX

PF 25-OCT-1999; 99WO-US25044.
XX
PR 23-OCT-1998; 98US-0105371.
PR 22-OCT-1999; 99US-0428082.
XX
PA (AMGE-) AMGEN INC.
XX
PI Feige U, Liu C, Cheetham J, Boone TC;
XX
DR WPI; 2000-350702/30.
XX
PT Novel composition of matter comprising an Fc domain and
PT pharmacologically active peptides, useful for treating cancer and
PT autoimmune diseases -
XX
PS Claim 13; Page 226; 608pp; English.
XX
CC The present invention describes composition of matter (I) comprising an
CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2,
CC -(L1)c-P1-(L2)d-P2-(L3)e-P³, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
CC where P1, P2, P3, and P4 = are each independently sequences of
CC pharmacologically active peptides; L1, L2, L3, and L4 = are each
CC independently linkers; and a, b, c, d, e, and f = are each independently
CC 0 or 1, provided that at least 1 of a and b is 1. The composition can
CC have cytostatic, antiasthmatic, thrombolytic and immunosuppressive
CC activities. DNAs, vectors and host cells from the present invention can
CC be used for producing pharmaceutical compositions. The compositions are
CC useful for treating cancer, asthma, thrombosis, or autoimmune diseases.
CC The use of an Fc domain (rather than a Fab domain) can provide a longer
CC half-life or incorporate functions such as Fc receptor binding, protein
CC A binding, complement fixation, and possibly placental transfer. AAA69443
CC to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid
CC sequences used in the exemplification of the present invention.
XX
SQ Sequence 40 AA;
Query Match 95.1%; Score 117; DB 21; Length 40;
Best Local Similarity 95.0%; Pred. No. 5.9e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTYSCHFGPLTWCKPQGG 20
RESULT 45
ABB72819
ID ABB72819 standard; Peptide; 40 AA.
XX
AC ABB72819;
XX
DT 05-APR-2002 (first entry)
XX
DE Erythropoietin (EPO) mimetic peptide SEQ ID NO:92.
XX
KW Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG;
KW EPO; erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
KW TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP;
KW TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
KW MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
KW cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
KW antianaemic; anorectic; antiinfertility; haemostatic; dermatological;
KW neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
KW cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
KW sleep disorder; neurological degenerative disease; anaemia;
KW thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
KW Fanconi's syndrome.
XX
OS Homo sapiens.
OS Synthetic.
XX

PN WO200183525-A2.
 XX 08-NOV-2001.
 PD
 XX
 PF 02-MAY-2001; 2001WO-US14310.
 XX
 PR 03-MAY-2000; 2000US-0563286.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Feige U, Liu C, Cheetham JC, Boone TC, Gudas JM;
 XX WPI; 2002-130313/17.
 DR
 XX Novel vehicle-peptide molecule or its multimers useful for treating
 PT inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
 PT diabetic retinopathy, obesity, sleep disorders and infertility -
 XX
 PS Claim 39; Page 41; 176pp; English.
 XX
 CC The present invention describes a vehicle-peptide molecule (I) or its
 CC multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
 CC cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,
 CC antianaemic, anorectic, antiinfertility, haemostatic, dermatological and
 CC neuroprotective activities. (I) can be used as a therapeutic or
 CC prophylactic agent as well as for screening purposes. (I) is useful for
 CC diagnosing diseases characterised by dysfunction of their associated
 CC protein of interest, for identifying normal or abnormal proteins of
 CC interest, as a part of diagnostic kit to detect the presence of their
 CC proteins of interest in a biological sample. Additionally, (I) is useful
 CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,
 CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
 CC infertility, and neurological degenerative diseases. (I), comprising
 CC EPO-mimetic compounds are useful for treating disorders characterised by
 CC low red blood cell levels such as anaemia. The TPO-mimetic comprising
 CC compounds are useful for treating conditions that involve an existing
 CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
 CC deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic
 CC tumour which result in thrombocytopaenia, systemic lupus erythematosus,
 CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777
 CC represent amino acid and nucleic acid sequences used in the
 CC exemplification of the present invention.
 XX
 SQ Sequence 40 AA;
 Query Match 95.1%; Score 117; DB 23; Length 40;
 Best Local Similarity 95.0%; Pred. No. 5.9e-09;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GGTASCHFGPLTWCKPQGG 20
 ||| ||||| ||||| |||||
 DB 1 GGTYSCHFGPLTWCKPQGG 20
 RESULT 46
 AAB17037
 ID AAB17037 standard; Peptide; 41 AA.
 XX
 AC AAB17037;
 XX
 DT 31-OCT-2000 (first entry)
 XX
 DE EPO-mimetic peptide sequence SEQ ID NO:93.
 XX
 KW Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
 KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
 KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist;
 KW MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
 KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
 KW vascular endothelial growth factor; matrix metalloproteinase;
 KW asthma; thrombosis; pharmaceutical.
 XX
 OS Synthetic.

XX WO200024782-A2.
 XX 04-MAY-2000.
 PD
 XX 25-OCT-1999; 99WO-US25044.
 XX
 PR 23-OCT-1998; 98US-0105371.
 PR 22-OCT-1999; 99US-0428082.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Feige U, Liu C, Cheetham J, Boone TC;
 XX WPI; 2000-350702/30.
 DR
 XX Novel composition of matter comprising an Fc domain and
 PT pharmacologically active peptides, useful for treating cancer and
 PT autoimmune diseases -
 XX
 PS Claim 13; Page 227; 608pp; English.
 XX
 CC The present invention describes composition of matter (I) comprising an
 CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
 CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
 CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2,
 CC -(L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
 CC where P1, P2, P3, and P4 = are each independently sequences of
 CC pharmacologically active peptides; L1, L2, L3, and L4 = are each
 CC independently linkers; and a, b, c, d, e, and f = are each independently
 CC 0 or 1, provided that at least 1 of a and b is 1. The composition can
 CC have cytostatic, antiasthmatic, thrombolytic and immunosuppressive
 CC activities. DNAs, vectors and host cells from the present invention can
 CC be used for producing pharmaceutical compositions. The compositions are
 CC useful for treating cancer, asthma, thrombosis, or autoimmune diseases.
 CC The use of an Fc domain (rather than a Fab domain) can provide a longer
 CC half-life or incorporate functions such as Fc receptor binding, protein
 CC A binding, complement fixation, and possibly placental transfer. AAA69443
 CC to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid
 CC sequences used in the exemplification of the present invention.
 XX
 SQ Sequence 41 AA;
 Query Match 95.1%; Score 117; DB 21; Length 41;
 Best Local Similarity 95.0%; Pred. No. 6.1e-09;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GGTASCHFGPLTWCKPQGG 20
 ||| ||||| ||||| |||||
 DB 1 GGTYSCHFGPLTWCKPQGG 20
 RESULT 47
 ABB72820
 ID ABB72820 standard; Peptide; 41 AA.
 XX
 AC ABB72820;
 XX
 DT 05-APR-2002 (first entry)
 XX
 DE Erythropoietin (EPO) mimetic peptide SEQ ID NO:93.
 XX
 KW Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG;
 KW EPO; erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
 KW TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP;
 KW TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
 KW MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
 KW cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
 KW antianaemic; anorectic; antiinfertility; haemostatic; dermatological;
 KW neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
 KW cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
 KW sleep disorder; neurological degenerative disease; anaemia;
 KW thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;

KW Fanconi's syndrome.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200183525-A2.
 XX
 PD 08-NOV-2001.
 XX
 PF 02-MAY-2001; 2001WO-US14310.
 XX
 PR 03-MAY-2000; 2000US-0563286.
 XX
 PA (AMGE-1) AMGEN INC.
 XX
 PI Feige U, Liu C, Cheetham JC, Boone TC, Gudas JM;
 XX
 DR WPI; 2002-130313/17.
 XX
 PT Novel vehicle-peptide molecule or its multimers useful for treating
 PT inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
 PT diabetic retinopathy, obesity, sleep disorders and infertility -
 XX
 PS Claim 39; Page 41; 176pp; English.
 XX
 CC The present invention describes a vehicle-peptide molecule (I) or its
 CC multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
 CC cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,
 CC antinaeemic, anorectic, antinfertility, haemostatic, dermatological and
 CC neuroprotective activities. (I) can be used as a therapeutic or
 CC prophylactic agent as well as for screening purposes. (I) is useful for
 CC diagnosing diseases characterised by dysfunction of their associated
 CC protein of interest, for identifying normal or abnormal proteins of
 CC interest, as a part of diagnostic kit to detect the presence of their
 CC proteins of interest in a biological sample. Additionally, (I) is useful
 CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,
 CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
 CC infertility, and neurological degenerative diseases. (I), comprising
 CC EPO-mimetic compounds are useful for treating disorders characterised by
 CC low red blood cell levels such as anaemia. The TPO-mimetic comprising
 CC compounds are useful for treating conditions that involve an existing
 CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
 CC deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic
 CC tumour which result in thrombocytopaenia, systemic lupus erythematosus,
 CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777
 CC represent amino acid and nucleic acid sequences used in the
 CC exemplification of the present invention.
 XX
 SQ Sequence 41 AA;
 Query Match 95.1%; Score 117; DB 23; Length 41;
 Best Local Similarity 95.0%; Pred. No. 6.1e-09;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GGTASCHFGPLTWCKPQGG 20
 Db 1 GGTYSCHFGPLTWCKPQGG 20
 RESULT 48
 AAY49902
 ID AAY49902 standard; peptide; 42 AA.
 XX
 AC AAY49902;
 XX
 DT 26-JAN-2000 (first entry)
 XX
 DE Erythropoietin receptor peptide.
 XX
 KW Erythropoietin receptor; screening; oligomerisation; PCR primer;
 KW cytokine receptor agonist; antagonist.
 XX
 OS Synthetic.

XX Key Location/Qualifiers
 FH Disulfide-bond 6..15
 FT Modified-site 22
 FT /label= bAla
 FT /note= "Beta-alanine"
 FT Disulfide-bond 28..37
 XX
 PN WO9953313-A1.
 XX
 PD 21-OCT-1999.
 XX
 PF 13-APR-1999; 99WO-JP01965.
 XX
 PR 14-APR-1998; 98JP-0102325.
 XX
 PA (CHUS) CHUGAI SEIYAKU KK.
 XX
 PI Higuchi M, Shimonaka Y, Esaki K;
 XX
 DR WPI; 1999-633837/54.
 XX
 PT Screening for promoters of oligomerization of receptor proteins or
 PT their fragments especially cytokine receptors -
 XX
 PS Example 6; Page 17; 36pp; Japanese.
 XX
 CC The present invention describes a method for screening substances for
 CC their ability to promote the oligomerisation of receptor proteins or
 CC their fragments, in which the protein or fragment is contacted with the
 CC test substance and the formation or non-formation of oligomers detected.
 CC The method is used for the identification of cytokine receptor agonists
 CC and antagonists and other cytokine activity regulators for use as drugs.
 CC The present sequence represents an erythropoietin receptor peptide
 CC from an example from the present invention.
 XX
 SQ Sequence 42 AA;
 Query Match 95.1%; Score 117; DB 20; Length 42;
 Best Local Similarity 95.0%; Pred. No. 6.2e-09;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GGTASCHFGPLTWCKPQGG 20
 Db 1 GGTYSCHFGPLTWCKPQGG 20
 RESULT 49
 AAB17039
 ID AAB17039 standard; Peptide; 46 AA.
 XX
 AC AAB17039;
 XX
 DT 31-OCT-2000 (first entry)
 XX
 DE EPO-mimetic peptide sequence SEQ ID NO:95.
 XX
 KW Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
 KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
 KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist;
 KW MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
 KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
 KW vascular endothelial growth factor; matrix metalloproteinase;
 KW asthma; thrombosis; pharmaceutical.
 XX
 OS Synthetic.
 XX
 PN WO200024782-A2.
 XX
 PD 04-MAY-2000.
 XX
 PF 25-OCT-1999; 99WO-US25044.
 XX

PR 23-OCT-1998; 98US-0105371.
PR 22-OCT-1999; 99US-0428082.
XX
PA (AMGE-) AMGEN INC.
XX
PI Feige U, Liu C, Cheetham J, Boone TC;
XX
DR WPI; 2000-350702/30.
XX
XX Novel composition of matter comprising an Fc domain and
PT pharmacologically active peptides, useful for treating cancer and
PT autoimmune diseases -

PS Claim 13; Page 228; 608pp; English.
XX
CC The present invention describes composition of matter (I) comprising an
CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2,
CC -(L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
CC where P1, P2, P3, and P4 = are each independently sequences of
CC pharmacologically active peptides; L1, L2, L3, and L4 = are each
CC independently linkers; and a, b, c, d, e, and f = are each independently
CC 0 or 1, provided that at least 1 of a and b is 1. The composition can
CC have cytostatic, antiasthmatic, thrombolytic and immunosuppressive
CC activities. DNAs, vectors and host cells from the present invention can
CC be used for producing pharmaceutical compositions. The compositions are
CC useful for treating cancer, asthma, thrombosis, or autoimmune diseases.
CC The use of an Fc domain (rather than a Fab domain) can provide a longer
CC half-life or incorporate functions such as Fc receptor binding, protein
CC A binding, complement fixation, and possibly placental transfer. AAAG9443
CC to AAA69526 and AAB18003 represent nucleotide and amino acid
CC sequences used in the exemplification of the present invention.

XX Sequence 46 AA;
SQ
Query Match 95.1%; Score 117; DB 21; Length 46;
Best Local Similarity 95.0%; Pred. No. 6.8e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
DB 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 50
AB872822
ID AB872822 standard; Peptide; 46 AA.
XX
AC AB872822;
XX
DT 05-APR-2002 (first entry)
XX
DE Erythropoietin (EPO) mimetic peptide SEQ ID NO:95.
XX
KW Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG;
KW EPO; erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
KW TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP;
KW TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
KW MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
KW cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
KW antianaemic; anorectic; antiinfertility; haemostatic; dermatological;
KW neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
KW cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
KW sleep disorder; neurological degenerative disease; anaemia;
KW thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
KW Fanconi's syndrome.
XX
OS Homo sapiens.
CS Synthetic.
XX
PN WO200183525-A2.

PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US14310.
XX
PR 03-MAY-2000; 2000US-0563286.
XX
PA (AMGE-) AMGEN INC.
XX
PI Feige U, Liu C, Cheetham JC, Boone TC, Gudas JM;
XX
DR WPI; 2002-130313/17.
XX
PT Novel vehicle-peptide molecule or its multimers useful for treating
PT inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
PT diabetic retinopathy, obesity, sleep disorders and infertility -
XX
PS Claim 39; Page 41; 176pp; English.
XX
CC The present invention describes a vehicle-peptide molecule (I) or its
CC multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
CC cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,
CC antianaemic, anorectic, antiinfertility, haemostatic, dermatological and
CC neuroprotective activities. (I) can be used as a therapeutic or
CC prophylactic agent as well as for screening purposes. (I) is useful for
CC diagnosing diseases characterised by dysfunction of their associated
CC protein of interest, for identifying normal or abnormal proteins of
CC interest, as a part of diagnostic kit to detect the presence of their
CC proteins of interest in a biological sample. Additionally, (I) is useful
CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,
CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
CC infertility, and neurological degenerative diseases. (I), comprising
CC EPO-mimetic compounds are useful for treating disorders characterised by
CC low red blood cell levels such as anaemia. The TPO-mimetic comprising
CC compounds are useful for treating conditions that involve an existing
CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
CC deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic
CC tumour which result in thrombocytopaenia, systemic lupus erythematosus,
CC and Fanconi's syndrome. AB872403 to AB873426 and ABL35695 to ABL35777
CC represent amino acid and nucleic acid sequences used in the
CC exemplification of the present invention.
XX
SQ Sequence 46 AA;

Query Match 95.1%; Score 117; DB 23; Length 46;
Best Local Similarity 95.0%; Pred. No. 6.8e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGTASCHFGPLTWCKPQGG 20
DB 1 GGTYSCHFGPLTWCKPQGG 20

Search completed: November 5, 2003, 19:05:31
Job time : 42 secs

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OM protein - protein search, using sw model

Run on: November 5, 2003, 19:04:44 ; Search time 21 Seconds
(without alignments)
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Title: US-09-863-600E-19
Perfect score: 123
Sequence: 1 GGFASCHFGPLTWCKPQGG 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Listing first 100 summaries

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Issued Patents AA:*
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5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	123	100.0	20	1	US-08-484-635-52
2	123	100.0	20	2	US-08-484-631-52
3	123	100.0	20	2	US-08-827-570-52
4	119	96.7	20	1	US-08-484-635-189
5	119	96.7	20	1	US-08-484-635-247
6	119	96.7	20	1	US-08-484-635-248
7	119	96.7	20	1	US-08-484-635-249
8	119	96.7	20	2	US-08-484-631-189
9	119	96.7	20	2	US-08-484-631-247
10	119	96.7	20	2	US-08-484-631-248
11	119	96.7	20	2	US-08-484-631-249
12	119	96.7	20	2	US-08-827-570-189
13	119	96.7	20	2	US-08-827-570-247
14	119	96.7	20	2	US-08-827-570-248
15	119	96.7	20	2	US-08-827-570-249
16	119	96.7	20	2	US-08-827-570-250
17	119	96.7	20	1	US-08-484-135-8
18	117	95.1	20	1	US-08-484-135-8
19	117	95.1	20	1	US-08-484-135-20
20	117	95.1	20	1	US-08-484-135-42
21	117	95.1	20	1	US-08-484-635-8
22	117	95.1	20	1	US-08-484-635-190
23	117	95.1	20	2	US-08-484-631-8
24	117	95.1	20	2	US-08-484-631-190
25	117	95.1	20	2	US-08-641-071-1
26	117	95.1	20	2	US-08-827-570-8
27	117	95.1	20	2	US-08-827-570-8

28	117	95.1	20	2	US-08-827-570-190	Sequence 190, App
29	117	95.1	20	3	US-08-905-310-2	Sequence 2, Appli
30	117	95.1	20	3	US-08-825-852-34	Sequence 34, Appl
31	117	95.1	20	3	US-08-786-690-1	Sequence 1, Appli
32	117	95.1	20	3	US-08-786-690-4	Sequence 4, Appli
33	117	95.1	20	3	US-09-052-888-34	Sequence 34, Appl
34	117	95.1	23	1	US-08-484-635-20	Sequence 20, Appl
35	117	95.1	23	2	US-08-484-631-20	Sequence 20, Appl
36	117	95.1	23	2	US-08-827-570-20	Sequence 20, Appl
37	112	91.1	20	1	US-08-484-635-192	Sequence 192, App
38	112	91.1	20	1	US-08-484-635-194	Sequence 194, App
39	112	91.1	20	2	US-08-484-631-192	Sequence 192, App
40	112	91.1	20	2	US-08-484-631-194	Sequence 194, App
41	112	91.1	20	2	US-08-827-570-192	Sequence 192, App
42	112	91.1	20	2	US-08-827-570-194	Sequence 194, App
43	111	90.2	20	1	US-08-484-635-18	Sequence 18, Appl
44	111	90.2	20	1	US-08-484-635-193	Sequence 193, App
45	111	90.2	20	2	US-08-484-631-18	Sequence 18, Appl
46	111	90.2	20	2	US-08-484-631-193	Sequence 193, App
47	111	90.2	20	2	US-08-827-570-18	Sequence 18, Appl
48	111	90.2	20	2	US-08-827-570-193	Sequence 193, App
49	109	88.6	20	1	US-08-484-635-191	Sequence 191, App
50	109	88.6	20	2	US-08-484-631-191	Sequence 191, App
51	109	88.6	20	2	US-08-827-570-191	Sequence 191, App
52	107	87.0	20	1	US-08-484-635-196	Sequence 196, App
53	107	87.0	20	1	US-08-484-635-251	Sequence 251, App
54	107	87.0	20	2	US-08-484-631-196	Sequence 196, App
55	107	87.0	20	2	US-08-484-631-251	Sequence 251, App
56	107	87.0	20	2	US-08-827-570-196	Sequence 196, App
57	107	87.0	20	2	US-08-827-570-251	Sequence 251, App
58	105	85.4	18	1	US-08-484-135-13	Sequence 13, Appl
59	105	85.4	18	1	US-08-484-635-13	Sequence 13, Appl
60	105	85.4	18	1	US-08-484-635-245	Sequence 245, App
61	105	85.4	18	2	US-08-484-631-13	Sequence 13, Appl
62	105	85.4	18	2	US-08-484-631-245	Sequence 245, App
63	105	85.4	18	2	US-08-827-570-13	Sequence 13, Appl
64	105	85.4	18	2	US-08-827-570-245	Sequence 245, App
65	105	85.4	18	3	US-08-905-310-7	Sequence 7, Appli
66	105	85.4	18	3	US-08-786-690-6	Sequence 6, Appli
67	103	83.7	20	1	US-08-484-635-195	Sequence 195, App
68	103	83.7	20	2	US-08-484-631-195	Sequence 195, App
69	103	83.7	20	2	US-08-827-570-195	Sequence 195, App
70	98.5	80.1	19	1	US-08-484-635-244	Sequence 244, App
71	98.5	80.1	19	2	US-08-484-631-244	Sequence 244, App
72	98.5	80.1	19	2	US-08-827-570-244	Sequence 244, App
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74	95	77.2	20	1	US-08-484-135-62	Sequence 62, Appl
75	95	77.2	20	1	US-08-484-635-37	Sequence 37, Appl
76	95	77.2	20	1	US-08-484-635-228	Sequence 228, App
77	95	77.2	20	2	US-08-484-631-37	Sequence 37, Appl
78	95	77.2	20	2	US-08-484-631-228	Sequence 228, App
79	95	77.2	20	2	US-08-827-570-37	Sequence 37, Appl
80	95	77.2	20	2	US-08-827-570-228	Sequence 228, App
81	93	75.6	16	1	US-08-484-635-197	Sequence 197, App
82	93	75.6	16	2	US-08-484-631-197	Sequence 197, App
83	93	75.6	16	2	US-08-827-570-197	Sequence 197, App
84	92	74.8	20	1	US-08-484-635-202	Sequence 202, App
85	92	74.8	20	2	US-08-484-631-202	Sequence 202, App
86	92	74.8	20	2	US-08-827-570-202	Sequence 202, App
87	90	73.2	20	1	US-08-484-135-25	Sequence 25, Appl
88	90	73.2	20	1	US-08-484-135-51	Sequence 51, Appl
89	90	73.2	20	1	US-08-484-635-55	Sequence 55, Appl
90	90	73.2	20	1	US-08-484-635-224	Sequence 224, App
91	90	73.2	20	2	US-08-484-631-55	Sequence 55, Appl
92	90	73.2	20	2	US-08-484-631-224	Sequence 224, App
93	90	73.2	20	2	US-08-827-570-55	Sequence 55, Appl
94	90	73.2	20	2	US-08-827-570-224	Sequence 224, App
95	89	72.4	20	1	US-08-484-135-10	Sequence 10, Appl
96	89	72.4	20	1	US-08-484-135-76	Sequence 76, Appl
97	89	72.4	20	1	US-08-484-635-10	Sequence 10, Appl
98	89	72.4	20	2	US-08-484-631-10	Sequence 10, Appl
99	89	72.4	20	2	US-08-827-570-10	Sequence 10, Appl
100	89	72.4	20	3	US-08-905-310-4	Sequence 4, Appli

ALIGNMENTS

```
RESULT 1
US-08-484-635-52
; Sequence 52, Application US/08484635
; Patent No. 5773569
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,635
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-484-635-52

Query Match 100.0%; Score 123; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
| | | | | | | | | | | | | | | | | |
Db 1 GGTASCHFGPLTWCKPQGG 20

RESULT 2
US-08-484-631-52
; Sequence 52, Application US/08484631
; Patent No. 5830851
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
```

```
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,631
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-484-631-52

Query Match 100.0%; Score 123; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
| | | | | | | | | | | | | | | | | |
Db 1 GGTASCHFGPLTWCKPQGG 20

RESULT 3
US-08-827-570-52
; Sequence 52, Application US/08827570
; Patent No. 5986047
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
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;
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/827,570
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,635
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-827-570-52

Query Match 100.0%; Score 123; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTASCHFGPLTWCKPQGG 20

RESULT 4
US-08-484-635-189
; Sequence 189, Application US/08484635
; Patent No. 5773569
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,635
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
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;
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 189:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-484-635-189

Query Match 96.7%; Score 119; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 8.4e-11;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTTSCHFGPLTWCKPQGG 20

RESULT 5
US-08-484-635-247
; Sequence 247, Application US/08484635
; Patent No. 5773569
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,635
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 247:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
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NAME/KEY: Modified-site
LOCATION: 4
OTHER INFORMATION: /product= "OTHER"
OTHER INFORMATION: /note= "Xaa = para-nitro-phenylalanine"
US-08-484-635-247

Query Match 96.7%; Score 119; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 8.4e-11;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| ||||| |||||
Db 1 GGTASCHFGPLTWCKPQGG 20

RESULT 6

US-08-484-635-248
; Sequence 248, Application US/08484635
; Patent No. 5773569
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,635
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/155,940
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 16528A-43-1-1
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 248:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 4
OTHER INFORMATION: /product= "OTHER"
OTHER INFORMATION: /note= "Xaa = para-amino-phenylalanine"

US-08-484-635-248
Query Match 96.7%; Score 119; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 8.4e-11;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| ||||| |||||
Db 1 GGTASCHFGPLTWCKPQGG 20

QY 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| ||||| |||||
Db 1 GGTASCHFGPLTWCKPQGG 20

RESULT 7

US-08-484-635-249
; Sequence 249, Application US/08484635
; Patent No. 5773569
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,635
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/155,940
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 16528A-43-1-1
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 249:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 4
OTHER INFORMATION: /product= "OTHER"
OTHER INFORMATION: /note= "Xaa = para-fluoro-phenylalanine"

US-08-484-635-249
Query Match 96.7%; Score 119; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 8.4e-11;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| ||||| |||||
Db 1 GGTASCHFGPLTWCKPQGG 20

RESULT 8
US-08-484-635-250
; Sequence 250, Application US/08484635

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; Patent No. 5773569
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,635
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 250:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /product= "OTHER"
; OTHER INFORMATION: /note= "Xaa = 3,5-dibromo-tyrosine"
US-09-484-635-250

Query Match 96.7%; Score 119; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 8.4e-11;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
   ||| ||||| ||||| |||||
Db 1 GGTASCHFGPLTWCKPQGG 20

RESULT 9
US-08-484-631-189
; Sequence 189, Application US/08484631
; Patent No. 5830851
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,635
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 250:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /product= "OTHER"
; OTHER INFORMATION: /note= "Xaa = 3,5-dibromo-tyrosine"
US-09-484-635-250

Query Match 96.7%; Score 119; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 8.4e-11;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
   ||| ||||| ||||| |||||
Db 1 GGTASCHFGPLTWCKPQGG 20

RESULT 9
US-08-484-631-189
; Sequence 189, Application US/08484631
; Patent No. 5830851
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
```

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; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,631
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 189:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-484-631-189

Query Match 96.7%; Score 119; DB 2; Length 20;
Best Local Similarity 95.0%; Pred. No. 8.4e-11;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
   ||| ||||| ||||| |||||
Db 1 GGTASCHFGPLTWCKPQGG 20

RESULT 10
US-08-484-631-247
; Sequence 247, Application US/08484631
; Patent No. 5830851
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,631
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/155,940
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 16528A-43-1-2
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 247:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 4
OTHER INFORMATION: /product= "OTHER"
OTHER INFORMATION: /note= "Xaa = para-nitro-phenylalanine"
US-08-484-631-247
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Query Match 96.7%; Score 119; DB 2; Length 20;
Best Local Similarity 95.0%; Pred. No. 8.4e-11;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
QY : GGTASCHFGPLTWCKPQGG 20
    ||| ||| ||| ||| ||| |||
Db 1 GGTXSCHEGPLTWCKPQGG 20
```

```
RESULT 11
US-08-484-631-248
Sequence 248, Application US/08484631
Patent No. 5830851
GENERAL INFORMATION:
APPLICANT: Wrighton, Nicholas C.
APPLICANT: Dower, William J.
APPLICANT: Chang, Ray S.
APPLICANT: Kashyap, Arun K.
APPLICANT: Jolliffe, Linda K.
APPLICANT: Johnson, Dana
APPLICANT: Mulcahy, Linda
TITLE OF INVENTION: Compounds and Peptides That Bind to the
TITLE OF INVENTION: Erythropoietin Receptor
NUMBER OF SEQUENCES: 259
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,631
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/155,940
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
```

```
NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 16528A-43-1-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 248:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 4
OTHER INFORMATION: /product= "OTHER"
OTHER INFORMATION: /note= "Xaa = para-amino-phenylalanine"
US-08-484-631-248
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Query Match 96.7%; Score 119; DB 2; Length 20;
Best Local Similarity 95.0%; Pred. No. 8.4e-11;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 GGTASCHFGPLTWCKPQGG 20
    ||| ||| ||| ||| ||| |||
Db 1 GGTXSCHEGPLTWCKPQGG 20
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```
RESULT 12
US-08-484-631-249
Sequence 249, Application US/08484631
Patent No. 5830851
GENERAL INFORMATION:
APPLICANT: Wrighton, Nicholas C.
APPLICANT: Dower, William J.
APPLICANT: Chang, Ray S.
APPLICANT: Kashyap, Arun K.
APPLICANT: Jolliffe, Linda K.
APPLICANT: Johnson, Dana
APPLICANT: Mulcahy, Linda
TITLE OF INVENTION: Compounds and Peptides That Bind to the
TITLE OF INVENTION: Erythropoietin Receptor
NUMBER OF SEQUENCES: 259
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,631
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/155,940
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 16528A-43-1-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 249:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
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; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /product= "OTHER"
; OTHER INFORMATION: /note= "Xaa = para-fluoro-phenylalanine"
US-08-484-631-249

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Query Match          96.7%; Score 119; DB 2; Length 20;
Best Local Similarity 95.0%; Pred. No. 8.4e-11;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      1 GGTASCHFGPLTWCKPQGG 20
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Db      1 GGTXSCHFGPLTWCKPQGG 20

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RESULT 13
US-08-484-631-250
; Sequence 250, Application US/08484631
; Patent No. 5830851
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Stuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,631
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 250:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /product= "OTHER"
; OTHER INFORMATION: /note= "Xaa = 3,5-dibromo-tyrosine"

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US-08-484-631-250
Query Match          96.7%; Score 119; DB 2; Length 20;
Best Local Similarity 95.0%; Pred. No. 8.4e-11;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      1 GGTASCHFGPLTWCKPQGG 20
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Db      1 GGTXSCHFGPLTWCKPQGG 20

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RESULT 14
US-08-827-570-189
; Sequence 189, Application US/08827570
; Patent No. 5986047
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Stuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/827,570
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,635
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 189:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-827-570-189

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Query Match          96.7%; Score 119; DB 2; Length 20;
Best Local Similarity 95.0%; Pred. No. 8.4e-11;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      1 GGTASCHFGPLTWCKPQGG 20
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Db      1 GGTXSCHFGPLTWCKPQGG 20

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RESULT 15


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US-08 827-570-247
; Sequence 247, Application US/08827570
; Patent No. 5986047
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/827,570
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,635
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 247:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /product= "OTHER"
; OTHER INFORMATION: /note= "Xaa = para-nitro-phenylalanine"
US-08-827-570-247
Query Match 96.7%; Score 119; DB 2; Length 20;
Best Local Similarity 95.0%; Pred. No. 8.4e-11;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTXSCHFGPLTWCKPQGG 20
RESULT 16
US-08-827-570-248
; Sequence 248, Application US/08827570
; Patent No. 5986047
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.

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; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/827,570
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,635
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 248:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
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; LOCATION: 4
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; OTHER INFORMATION: /note= "Xaa = para-amino-phenylalanine"
US-08-827-570-248
Query Match 96.7%; Score 119; DB 2; Length 20;
Best Local Similarity 95.0%; Pred. No. 8.4e-11;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTXSCHFGPLTWCKPQGG 20
RESULT 17
US-08-827-570-249
; Sequence 249, Application US/08827570
; Patent No. 5986047
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259

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;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/827,570
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,635
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 249:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
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; OTHER INFORMATION: /note= "Xaa = para-fluoro-phenylalanine"
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; Query Match 96.7%; Score 119; DB 2; Length 20;
; Best Local Similarity 95.0%; Pred. No. 8.4e-11;
; Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; QY 1 GGTASCHFGPLTWCKPQGG 20
; Db 1 GGTXSCHFGPLTWCKPQGG 20
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; RESULT 18
; US-08-827-570-250
; Sequence 250, Application US/08827570
; Patent No. 5986047
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
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;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/827,570
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,635
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 250:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /product= "OTHER"
; OTHER INFORMATION: /note= "Xaa = 3,5-dibromo-tyrosine"
;
; US-08-827-570-250
;
; Query Match 96.7%; Score 119; DB 2; Length 20;
; Best Local Similarity 95.0%; Pred. No. 8.4e-11;
; Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; QY 1 GGTASCHFGPLTWCKPQGG 20
; Db 1 GGTXSCHFGPLTWCKPQGG 20
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; RESULT 19
; US-08-484-135-8
; Sequence 8, Application US/08484135
; Patent No. 5767078
; GENERAL INFORMATION:
; APPLICANT: Johnson, Dana L
; APPLICANT: Zivin, Robert A
; TITLE OF INVENTION: AGONIST PEPTIDE DIMERS
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Frank S. DiGiglio
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,135
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9594
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-484-135-8

Query Match 95.1%; Score 117; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.6e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
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Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 20
US-08-484-135-20
Sequence 20, Application US/08484135
Patent No. 5767078
GENERAL INFORMATION:
APPLICANT: Johnson, Dana L
APPLICANT: Zivin, Robert A
TITLE OF INVENTION: AGONIST PEPTIDE DIMERS
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: Frank S. DiGiglio
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: U.S.A..
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,135
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: DiGiglio, Frank S
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9594
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-484-135-20

Query Match 95.1%; Score 117; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.6e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
||| |||||
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 21
US-08-484-135-42

Sequence 42, Application US/08484135
Patent No. 5767078
GENERAL INFORMATION:
APPLICANT: Johnson, Dana L
APPLICANT: Zivin, Robert A
TITLE OF INVENTION: AGONIST PEPTIDE DIMERS
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: Frank S. DiGiglio
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: U.S.A..
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,135
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: DiGiglio, Frank S
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9594
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-484-135-42

Query Match 95.1%; Score 117; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.6e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
||| |||||
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 22
US-08-484-635-8
Sequence 8, Application US/08484635
Patent No. 5773569
GENERAL INFORMATION:
APPLICANT: Wrighton, Nicholas C.
APPLICANT: Dower, William J.
APPLICANT: Chang, Ray S.
APPLICANT: Kashyap, Arun K.
APPLICANT: Jolliffe, Linda K.
APPLICANT: Johnson, Dana
APPLICANT: Mulcahy, Linda
TITLE OF INVENTION: Compounds and Peptides That Bind to the
TITLE OF INVENTION: Erythropoietin Receptor
NUMBER OF SEQUENCES: 259
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,635
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-484-635-8

Query Match          95.1%; Score 117; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.6e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGTASCHFGPLTWCKPQGG 20
Db      1 GGTYSCHFGPLTWCKPQGG 20

RESULT 23
US-08-484-635-190
; Sequence 190, Application US/08484635
; Patent No. 5773569
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,635
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-1
; TELECOMMUNICATION INFORMATION:

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; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 190:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-484-635-190

Query Match          95.1%; Score 117; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.6e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGTASCHFGPLTWCKPQGG 20
Db      1 GGTFSCHFGPLTWCKPQGG 20

RESULT 24
US-08-484-631-8
; Sequence 8, Application US/08484631
; Patent No. 5830851
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,631
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-484-631-8

Query Match          95.1%; Score 117; DB 2; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.6e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/827,570
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/484,635
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/155,940
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 16528A-43-i-1
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-827-570-8

Query Match 95.1%; Score 117; DB 2; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.6e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 28
US-08-827-570-190
; Sequence 190, Application US/08827570
; Patent No. 5986047
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,635
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/155,940

FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 16528A-43-i-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 190:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-827-570-190

Query Match 95.1%; Score 117; DB 2; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.6e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTFSCHFGPLTWCKPQGG 20

RESULT 29
US-08-905-310-2
; Sequence 2, Application US/08905310
; Patent No. 6077939
; GENERAL INFORMATION:
; APPLICANT: Wei, Ziping
; APPLICANT: Menon-Rudolph, Sunitha
; APPLICANT: Ghosh-Dastidar, Pradip
; TITLE OF INVENTION: Polypeptides Having a Single Covalently Bound
; TITLE OF INVENTION: N-Terminal Water-Soluble Polymer, and Related Methods,
; TITLE OF INVENTION: Compositions and Kits
; FILE REFERENCE: SEQUENCE LISTING ORT 843
; CURRENT APPLICATION NUMBER: US/08/905,310
; CURRENT FILING DATE: 1997-08-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism:peptide fragment
US-08-905-310-2

Query Match 95.1%; Score 117; DB 3; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.6e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 30
US-08-825-852-34
; Sequence 34, Application US/08825852
; Patent No. 6121416
; GENERAL INFORMATION:
; APPLICANT: Clark, Ross G1
; APPLICANT: Lowman, Henry B.
; APPLICANT: Robinson, Iain C.A.F.
; TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules
; NUMBER OF SEQUENCES: 79
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco

```

; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; FILING DATE: 04-Apr-1997
; APPLICATION NUMBER: US/08/825,852
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: P1071
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1896
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-825-852-34

```

```

Query Match 95.1%; Score 117; DB 3; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.6e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTYSCHFGPLTWCKPQGG 20

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RESULT 31
US-08-786-690-1
; Sequence 1, Application US/08786690
; Patent No. 6221608
; GENERAL INFORMATION:
; APPLICANT: Middleton, Steven
; APPLICANT: Johnson, Dana
; APPLICANT: McMahon, Frank
; APPLICANT: Mulkahy, Linda
; APPLICANT: Jolliffe, Linda
; TITLE OF INVENTION: METHOD FOR PURIFICATION AND USE OF
; TITLE OF INVENTION: ERYTHROPOIETIN BINDING PROTEIN
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Johnson & Johnson
; STREET: One Johnson & Johnson Plaza
; CITY: New Brunswick
; STATE: NJ
; COUNTRY: USA
; ZIP: 08933-7003
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/786,690
; FILING DATE: 08 August 1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Wallen, John W.
; REGISTRATION NUMBER: 35,403
; REFERENCE/DOCKET NUMBER: ORT-82;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-524-2806
; TELEFAX: 732-524-2808
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:

```

```

; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ANTI-SENSE: NO
; US-08-786-690-1

```

```

Query Match 95.1%; Score 117; DB 3; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.6e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTYSCHFGPLTWCKPQGG 20

```

```

RESULT 32
US-08-786-690-4
; Sequence 4, Application US/08786690
; Patent No. 6221608
; GENERAL INFORMATION:
; APPLICANT: Middleton, Steven
; APPLICANT: Johnson, Dana
; APPLICANT: McMahon, Frank
; APPLICANT: Mulkahy, Linda
; APPLICANT: Jolliffe, Linda
; TITLE OF INVENTION: METHOD FOR PURIFICATION AND USE OF
; TITLE OF INVENTION: ERYTHROPOIETIN BINDING PROTEIN
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Johnson & Johnson
; STREET: One Johnson & Johnson Plaza
; CITY: New Brunswick
; STATE: NJ
; COUNTRY: USA
; ZIP: 08933-7003
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/786,690
; FILING DATE: 08 August 1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Wallen, John W.
; REGISTRATION NUMBER: 35,403
; REFERENCE/DOCKET NUMBER: ORT-821
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-524-2806
; TELEFAX: 732-524-2808
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ANTI-SENSE: NO
; US-08-786-690-4

```

```

Query Match 95.1%; Score 117; DB 3; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.6e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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```

Qy 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTYSCHFGPLTWCKPQGG 20

```

RESULT 33


```
US-09-052-888-34
; Sequence 34, Application US/09052888
; Patent No. 6251865
; GENERAL INFORMATION:
; APPLICANT: Clark, Ross G1
; APPLICANT: Lowman, Henry B.
; APPLICANT: Robinson, Iain C.A.F.
; TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules
; NUMBER OF SEQUENCES: 109
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/052.888
; FILING DATE: 31-Mar-1998
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: Pl071p1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1896
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
US-09-052-888-34

Query Match 95.1%; Score 117; DB 3; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.6e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 34
US-08-484-635-20
; Sequence 20, Application US/08484635
; Patent No. 5773569
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,631
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-2
; TELECOMMUNICATION INFORMATION:
```

```
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,635
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-08-484-635-20

Query Match 95.1%; Score 117; DB 1; Length 23;
Best Local Similarity 95.0%; Pred. No. 1.9e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 35
US-08-484-631-20
; Sequence 20, Application US/08484631
; Patent No. 5830851
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,631
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-2
; TELECOMMUNICATION INFORMATION:
```

TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-484-631-20

Query Match 95.1%; Score 117; DB 2; Length 23;
Best Local Similarity 95.0%; Pred. No. 1.9e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| ||||| |||||
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 36

US-08-827-570-20
; Sequence 20, Application US/08827570
; Patent No. 5986047
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/827,570
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,635
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-827-570-20

Query Match 95.1%; Score 117; DB 2; Length 23;

Best Local Similarity 95.0%; Pred. No. 1.9e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| ||||| |||||
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 37

US-08-484-635-192
; Sequence 192, Application US/08484635
; Patent No. 5773569
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,635
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 192:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-484-635-192

Query Match 91.1%; Score 112; DB 1; Length 20;

Best Local Similarity 90.0%; Pred. No. 8.4e-10;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| ||||| |||||
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 38

US-08-484-635-194
; Sequence 194, Application US/08484635
; Patent No. 5773569
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.

```
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,635
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 194:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-484-635-194

Query Match 91.1%; Score 112; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 8.4e-10;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
   ||| ||||| ||||| |||
Db 1 GGTYSCHFGPATWCKPQGG 20

RESULT 39
US-08-484-631-192
; Sequence 192, Application US/08484631
; Patent No. 5830851
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
```

```
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,631
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 192:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-484-631-192

Query Match 91.1%; Score 112; DB 2; Length 20;
Best Local Similarity 90.0%; Pred. No. 8.4e-10;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
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Db 1 GGTYSCHFGPLAWCKPQGG 20

RESULT 40
US-08-484-631-194
; Sequence 194, Application US/08484631
; Patent No. 5830851
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,631
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
```

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;
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 194:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-484-631-194

Query Match          91.1%; Score 112; DB 2; Length 20;
Best Local Similarity 90.0%; Pred. NO. 8.4e-10;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GGTASCHFGPLTWVCKPQGG 20
Db      : GGTYSCHFGPATWVCKPQGG 20
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RESULT 4:
US-08-827-570-192
; Sequence 192, Application US/08827570
; Patent No. 5986047
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/827,570
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,635
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-1
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 192:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-827-570-194

Query Match          91.1%; Score 112; DB 2; Length 20;
Best Local Similarity 90.0%; Pred. NO. 8.4e-10;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GGTASCHFGPLTWVCKPQGG 20
Db      : GGTYSCHFGPATWVCKPQGG 20
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; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-827-570-192

Query Match          91.1%; Score 112; DB 2; Length 20;
Best Local Similarity 90.0%; Pred. NO. 8.4e-10;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GGTASCHFGPLTWVCKPQGG 20
Db      1 GGTYSCHFGPLAWVCKPQGG 20
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RESULT 42
US-08-827-570-194
; Sequence 194, Application US/08827570
; Patent No. 5986047
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/827,570
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,635
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 194:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-827-570-194

Query Match          91.1%; Score 112; DB 2; Length 20;
Best Local Similarity 90.0%; Pred. NO. 8.4e-10;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GGTASCHFGPLTWVCKPQGG 20
Db      1 GGTYSCHFGPATWVCKPQGG 20
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RESULT 43
US-08-484-635-18
; Sequence 18, Application US/08484635
; Patent No. 5773569
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,635
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /product= "OTHER"
; OTHER INFORMATION: /note= "Xaa = N-acetyl-glycine"
US-08-484-635-18
Query Match 90.2%; Score 111; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 1.2e-09;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GTASCHFGPLTWCKPQGG 20
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Db 2 GTYSCHFGPLTWCKPQGG 20

RESULT 44
US-08-484-635-193
; Sequence 193, Application US/08484635
; Patent No. 5773569
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
```

```
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,635
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 193:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-484-635-193
Query Match 90.2%; Score 111; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.2e-09;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
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Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 45
US-08-484-631-18
; Sequence 18, Application US/08484631
; Patent No. 5830851
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,631
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /product= "OTHER"
; OTHER INFORMATION: /note= "Xaa = N-acetyl-glycine"
;
; US-08-484-631-18
;
; Query Match 90.2%; Score 111; DB 2; Length 20;
; Best Local Similarity 94.7%; Pred. No. 1.2e-09;
; Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; QY 2 GTASCHFGPLTWCKPQGG 20
; Db 2 GTYSCHFAPLTWCKPQGG 20
;
; RESULT 46
; US-08-484-631-193
; Sequence 193, Application US/08484631
; Patent No. 583085;
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,631
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 193:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
; US-08-484-631-193
;
; Query Match 90.2%; Score 111; DB 2; Length 20;
; Best Local Similarity 90.0%; Pred. No. 1.2e-09;
; Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;
; QY 1 GGTASCHFGPLTWCKPQGG 20
; Db 1 GGTYSCHFAPLTWCKPQGG 20
;
; RESULT 47
; US-08-827-570-18
; Sequence 18, Application US/08827570
; Patent No. 5986047
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/827,570
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,635
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
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; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /product= "OTHER"
; OTHER INFORMATION: /note= "Xaa = N-acetyl-glycine"
US-08-827-570-18

Query Match 90.2%; Score 111; DB 2; Length 20;
Best Local Similarity 94.7%; Pred. No. 1.2e-09;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GTASCHFGPLTWCKPQGG 20
Db 2 GTYSCHEGPLTWCKPQGG 20

RESULT 48
US-08-827-570-193
; Sequence 193, Application US/08827570
; Patent No. 5986047
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/827,570
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,635
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 193:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-827-570-193

Query Match 90.2%; Score 111; DB 2; Length 20;
Best Local Similarity 94.7%; Pred. No. 1.2e-09;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GTASCHFGPLTWCKPQGG 20
Db 2 GTYSCHEGPLTWCKPQGG 20

RESULT 49
US-08-484-635-191
; Sequence 191, Application US/08484635
; Patent No. 5773569
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,635
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 191:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-484-635-191

Query Match 88.6%; Score 109; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.3e-09;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTYSCHFAPLTWCKPQGG 20

RESULT 50
US-08-484-631-191
; Sequence 191, Application US/08484631
; Patent No. 5830851
; GENERAL INFORMATION:
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APPLICANT: Wrighton, Nicholas C.
APPLICANT: Dower, William J.
APPLICANT: Chang, Ray S.
APPLICANT: Kashyap, Arun K.
APPLICANT: Jolliffe, Linda K.
APPLICANT: Johnson, Dana
APPLICANT: Mulcahy, Linda
TITLE OF INVENTION: Compounds and Peptides That Bind to the
TITLE OF INVENTION: Erythropoietin Receptor
NUMBER OF SEQUENCES: 259
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,631
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/155,940
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 16528A-43-1-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 191:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-484-631-191

Query Match 88.6%; Score 109; DB 2; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.3e-09;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
DB 1 GGTYSCHFGALTWCKPQGG 20

Search completed: November 5, 2003, 19:07:50
Job time : 22 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 5, 2003, 19:06:49 ; Search time 29 Seconds
(without alignments)
118.448 Million cell updates/sec

Title: US-09-863-600E-19
Perfect score: 123
Sequence: 1 GGTASCHFGPLTWCKPQGG 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 644079 seqs, 171749292 residues

Total number of hits satisfying chosen parameters: 644079

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Published Applications AA:*

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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	119	96.7	20	12	US-09-863-600E-38
5	119	96.7	20	12	US-09-863-600E-39
6	119	96.7	20	12	US-09-863-600E-40
7	119	96.7	20	12	US-09-863-600E-41
8	119	96.7	20	12	US-09-863-600E-42
9	117	95.1	20	11	US-09-858-935B-66
10	117	95.1	20	12	US-09-863-600E-8
11	117	95.1	20	12	US-09-863-600E-30
12	112	91.1	20	12	US-09-863-600E-32
13	112	91.1	20	12	US-09-863-600E-33
14	111	90.2	20	12	US-09-863-600E-20
15	111	90.2	20	12	US-09-863-600E-43

16	109	88.6	20	12	US-09-863-600E-31	Sequence 31, Appl
17	109	88.6	20	12	US-09-863-600E-36	Sequence 36, Appl
18	107	87.0	20	12	US-09-863-600E-35	Sequence 35, Appl
19	105	85.4	18	12	US-09-863-600E-13	Sequence 13, Appl
20	105	85.4	18	12	US-09-863-600E-22	Sequence 22, Appl
21	103	83.7	20	12	US-09-863-600E-34	Sequence 34, Appl
22	98.5	80.1	19	12	US-09-863-600E-21	Sequence 21, Appl
23	93	75.6	16	12	US-09-863-600E-23	Sequence 23, Appl
24	92	74.8	20	12	US-09-863-600E-46	Sequence 46, Appl
25	89	72.4	20	12	US-09-863-600E-10	Sequence 10, Appl
26	89	72.4	20	12	US-09-863-600E-44	Sequence 44, Appl
27	85	69.1	14	12	US-09-863-600E-24	Sequence 24, Appl
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31	81	65.9	20	12	US-09-863-600E-14	Sequence 14, Appl
32	78	63.4	12	12	US-09-863-600E-18	Sequence 18, Appl
33	78	63.4	12	12	US-10-271-343-14	Sequence 14, Appl
34	78	63.4	13	12	US-09-863-600E-16	Sequence 16, Appl
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36	73	59.3	12	12	US-09-863-600E-25	Sequence 25, Appl
37	70	56.9	13	12	US-09-863-600E-26	Sequence 26, Appl
38	69	56.1	11	12	US-09-863-600E-17	Sequence 17, Appl
39	68	55.3	19	12	US-09-863-600E-12	Sequence 12, Appl
40	66	53.7	20	12	US-09-863-600E-7	Sequence 7, Appli
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44	53	43.1	22	12	US-09-863-600E-15	Sequence 15, Appl
45	51	41.5	8	12	US-09-863-600E-28	Sequence 28, Appl
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47	51	41.5	23	11	US-09-858-935B-46	Sequence 46, Appl
48	51	41.5	97	11	US-09-858-935B-47	Sequence 47, Appl
49	49	39.8	24	9	US-09-864-761-40377	Sequence 40377, A
50	48	39.0	42	9	US-09-864-761-48118	Sequence 48118, A
51	47	38.2	18	11	US-09-858-935B-108	Sequence 108, App
52	46.5	37.8	73	11	US-09-910-082A-301	Sequence 301, App
53	46	37.4	12	12	US-10-271-343-15	Sequence 15, Appl
54	46	37.4	15	11	US-09-858-935B-26	Sequence 26, Appl
55	46	37.4	19	11	US-09-858-935B-27	Sequence 27, Appl
56	46	37.4	19	11	US-09-858-935B-33	Sequence 33, Appl
57	46	37.4	293	12	US-10-145-206-123	Sequence 123, App
58	45.5	37.0	75	12	US-10-139-272-75	Sequence 75, Appl
59	45.5	37.0	469	11	US-09-984-130-41	Sequence 41, Appl
60	45.5	37.0	469	12	US-09-836-353A-41	Sequence 41, Appl
61	45.5	37.0	494	11	US-09-984-130-30	Sequence 30, Appl
62	45.5	37.0	494	12	US-09-836-353A-30	Sequence 30, Appl
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73	45	36.6	18	11	US-09-858-935B-38	Sequence 38, Appl
74	45	36.6	18	11	US-09-858-935B-39	Sequence 39, Appl
75	45	36.6	21	11	US-09-858-935B-40	Sequence 40, Appl
76	45	36.6	21	11	US-09-858-935B-42	Sequence 42, Appl
77	45	36.6	28	11	US-09-932-613-165	Sequence 165, App
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79	45	36.6	290	9	US-09-764-853-513	Sequence 513, App
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87	44	35.8	14	11	US-09-858-935B-50	Sequence 50, Appl
88	44	35.8	58	15	US-10-106-698-5090	Sequence 5090, Ap

89 44 35.8 82 9 US-09-729-835-114 Sequence 114, App
90 44 35.8 102 11 US-09-746-783-21 Sequence 21, Appl
91 44 35.8 166 15 US-10-103-313-573 Sequence 573, App
92 44 35.8 460 15 US-10-156-761-8851 Sequence 8851, Ap
93 43 35.0 14 11 US-09-858-935B-31 Sequence 31, Appl
94 43 35.0 14 11 US-09-858-935B-32 Sequence 32, Appl
95 43 35.0 14 11 US-09-858-935B-34 Sequence 34, Appl
96 43 35.0 14 11 US-09-858-935B-51 Sequence 51, Appl
97 43 35.0 14 11 US-09-858-935B-138 Sequence 138, App
98 43 35.0 16 12 US-09-863-600E-4 Sequence 4, Appli
99 43 35.0 16 12 US-09-863-600E-5 Sequence 5, Appli
100 43 35.0 16 12 US-09-863-600E-6 Sequence 6, Appli

ALIGNMENTS

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RESULT 1
US-09-863-600E-19
; Sequence 19, Application US/09863600E
; Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-09-863-600E-19

Query Match 100.0%; Score 123; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
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Db 1 GGTASCHFGPLTWCKPQGG 20

RESULT 2
US-09-863-600E-29
; Sequence 29, Application US/09863600E
; Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29

Query Match 100.0%; Score 123; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GGTASCHFGPLTWCKPQGG 20

RESULT 3
US-09-863-600E-37
; Sequence 37, Application US/09863600E
; Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 37
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-09-863-600E-37

Query Match 96.7%; Score 119; DB 12; Length 20;
Best Local Similarity 95.0%; Pred. No. 5.8e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
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Db 1 GGTASCHFGPLTWCKPQGG 20

RESULT 4
US-09-863-600E-38
; Sequence 38, Application US/09863600E
; Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
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; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-09-863-600E-29

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Best Local Similarity 95.0%; Pred. No. 5.8e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 1 GGTASCHFGPLTWCKPQGG 20

RESULT 3
US-09-863-600E-37
; Sequence 37, Application US/09863600E
; Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 37
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-09-863-600E-37

Query Match 96.7%; Score 119; DB 12; Length 20;
Best Local Similarity 95.0%; Pred. No. 5.8e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
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Db 1 GGTASCHFGPLTWCKPQGG 20

RESULT 4
US-09-863-600E-38
; Sequence 38, Application US/09863600E
; Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
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; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: Xaa is p-NO2-Phe
US-09-863-600E-38

Query Match          96.7%; Score 119; DB 12; Length 20;
Best Local Similarity 95.0%; Pred. No. 5.8e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGTASCHFGPLTWCKPQGG 20
Db      1 GGTXSCHFGPLTWCKPQGG 20

RESULT 5
US-09-863-600E-39
; Sequence 39, Application US/09863600E
; Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 39
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: Xaa is p-NH2-Phe
US-09-863-600E-39

Query Match          96.7%; Score 119; DB 12; Length 20;
Best Local Similarity 95.0%; Pred. No. 5.8e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGTASCHFGPLTWCKPQGG 20
Db      1 GGTXSCHFGPLTWCKPQGG 20

RESULT 6
US-09-863-600E-40
; Sequence 40, Application US/09863600E
; Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
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; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: Xaa is p-F-Phe
US-09-863-600E-40

Query Match          96.7%; Score 119; DB 12; Length 20;
Best Local Similarity 95.0%; Pred. No. 5.8e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGTASCHFGPLTWCKPQGG 20
Db      1 GGTXSCHFGPLTWCKPQGG 20

RESULT 7
US-09-863-600E-41
; Sequence 41, Application US/09863600E
; Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 41
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: Xaa is p-I-Phe
US-09-863-600E-41

Query Match          96.7%; Score 119; DB 12; Length 20;
Best Local Similarity 95.0%; Pred. No. 5.8e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGTASCHFGPLTWCKPQGG 20
Db      1 GGTXSCHFGPLTWCKPQGG 20

RESULT 8
US-09-863-600E-42
; Sequence 42, Application US/09863600E
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; Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 42
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
; NAME/KEY: misc feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: Xaa is 3,5-dibromo-Tyr
US-09-863-600E-42

Query Match 96.7%; Score 119; DB 12; Length 20;
Best Local Similarity 95.0%; Pred. No. 5.8e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWVCKPQGG 20
||| ||||| ||||| |||||
Db 1 GGTXSCHFGPLTWVCKPQGG 20

RESULT 9
US-09-858-935B-66
; Sequence 66, Application US/09858935B
; Publication No. US20030069177A1
; GENERAL INFORMATION:
; APPLICANT: Dubaqui, Yves
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Lowman, Henry B.
; TITLE OF INVENTION: METHOD FOR TREATING CARTILAGE DISORDERS
; FILE REFERENCE: P1794R1
; CURRENT APPLICATION NUMBER: US/09/858,935B
; CURRENT FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 60/248,985
; PRIOR FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: US 60/204,490
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 66
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-09-858-935B-66

Query Match 95.1%; Score 117; DB 11; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.1e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWVCKPQGG 20
||| ||||| ||||| |||||
Db 1 GGTYSCHFGPLTWVCKPQGG 20

RESULT 10
US-09-863-600E-8

; Sequence 8, Application US/09863600E
; Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-09-863-600E-8

Query Match 95.1%; Score 117; DB 12; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.1e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWVCKPQGG 20
||| ||||| ||||| |||||
Db 1 GGTYSCHFGPLTWVCKPQGG 20

RESULT 11
US-09-863-600E-30
; Sequence 30, Application US/09863600E
; Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 30
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-09-863-600E-30

Query Match 95.1%; Score 117; DB 12; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.1e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWVCKPQGG 20
||| ||||| ||||| |||||
Db 1 GGTFSCHFGPLTWVCKPQGG 20

RESULT 12
US-09-863-600E-32
; Sequence 32, Application US/09863600E

```
; Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 32
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-09-863-600E-32
```

```
Query Match          91.1%; Score 112; DB 12; Length 20;
Best Local Similarity 90.0%; Pred. No. 5.5e-09;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1 GGTASCHFGPLTWCKPQGG 20
   ||||| ||||| ||||| |||||
DB 1 GGTYSCHFGPATWCKPQGG 20
```

```
RESULT 13
US-09-863-600E-33
; Sequence 33, Application US/09863600E
; Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 33
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-09-863-600E-33
```

```
Query Match          91.1%; Score 112; DB 12; Length 20;
Best Local Similarity 90.0%; Pred. No. 5.5e-09;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1 GGTASCHFGPLTWCKPQGG 20
   ||||| ||||| ||||| |||||
DB 1 GGTYSCHFGPLAWCKPQGG 20
```

```
RESULT 14
US-09-863-600E-20
; Sequence 20, Application US/09863600E
; Publication No. US20030130197A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-09-863-600E-20
```

```
Query Match          90.2%; Score 111; DB 12; Length 20;
Best Local Similarity 90.0%; Pred. No. 7.6e-09;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1 GGTASCHFGPLTWCKPQGG 20
   ||||| ||||| ||||| |||||
DB 1 GGTYSCHFGAPLTWCKPQGG 20
```

```
RESULT 15
US-09-863-600E-43
; Sequence 43, Application US/09863600E
; Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
; NAME/KEY: misc_feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: Xaa is Ac-Gly
US-09-863-600E-43
```

```
Query Match          90.2%; Score 111; DB 12; Length 20;
Best Local Similarity 94.7%; Pred. No. 7.6e-09;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 2 GTASCHFGPLTWCKPQGG 20
   ||||| ||||| ||||| |||||
DB 2 GTYSCHFGPLTWCKPQGG 20
```

```
RESULT 16
```

US-09-863-600E-31
; Sequence 31, Application US/09863600E
; Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 31
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-09-863-600E-31

Query Match 88.6%; Score 109; DB 12; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.4e-08;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWVCKPQGG 20
||| |||| |||| |||| ||||
Db 1 GGTYSCHFGALTWVCKPQGG 20

RESULT 17
US-09-863-600E-36
; Sequence 36, Application US/09863600E
; Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 36
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-09-863-600E-36

Query Match 88.6%; Score 109; DB 12; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.4e-08;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWVCKPQGG 20
||| |||| |||| |||| ||||
Db 1 GGTYSCHFGPLTWVCKAQQG 20

RESULT 18
US-09-863-600E-35

; Sequence 35, Application US/09863600E
; Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-09-863-600E-35

Query Match 87.0%; Score 107; DB 12; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.7e-08;
Matches 18; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWVCKPQGG 20
||| |||| |||| |||| ||||
Db 1 GGTYSCHFGPLTFVCKPQGG 20

RESULT 19
US-09-863-600E-13
; Sequence 13, Application US/09863600E
; Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-09-863-600E-13

Query Match 85.4%; Score 105; DB 12; Length 18;
Best Local Similarity 94.4%; Pred. No. 4.7e-08;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWVCKPQ 18
||| |||| |||| |||| ||||
Db 1 GGTYSCHFGPLTWVCKPQ 18

RESULT 20
US-09-863-600E-22
; Sequence 22, Application US/09863600E

; Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-09-863-600E-22

Query Match 85.4%; Score 105; DB 12; Length 18;
Best Local Similarity 94.4%; Pred. No. 4.7e-08;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TASCHEGFLTWCKPQG 20
| | | | | | | | | | | | | | | | | |
Db 1 TYSCHFGPLTWCKPQG 18

RESULT 21
US-09-863-600E-34
; Sequence 34, Application US/09863600E
; Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-09-863-600E-34

Query Match 83.7%; Score 103; DB 12; Length 20;
Best Local Similarity 90.0%; Pred. No. 9.9e-08;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQG 20
| | | | | | | | | | | | | | | | | |
Db 1 GGTYSCHFGPLTAVCKPQG 20

RESULT 22
US-09-863-600E-21
; Sequence 21, Application US/09863600E
; Publication No. US20030130197A1

; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-09-863-600E-21

Query Match 80.1%; Score 98.5; DB 12; Length 19;
Best Local Similarity 90.0%; Pred. No. 4e-07;
Matches 18; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 GGTASCHFGPLTWCKPQG 20
| | | | | | | | | | | | | | | | | |
Db 1 GGTYSCHFGPLTWCKPQG 19

RESULT 23
US-09-863-600E-23
; Sequence 23, Application US/09863600E
; Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-09-863-600E-23

Query Match 75.6%; Score 93; DB 12; Length 16;
Best Local Similarity 93.8%; Pred. No. 2e-06;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TASCHEGFLTWCKPQ 18
| | | | | | | | | | | | | | | | | |
Db 1 TYSCHFGPLTWCKPQ 16

RESULT 24
US-09-863-600E-46
; Sequence 46, Application US/09863600E
; Publication No. US20030130197A1
; GENERAL INFORMATION:

; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 46
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-09-863-600E-46

Query Match 74.8%; Score 92; DB 12; Length 20;
Best Local Similarity 85.0%; Pred. No. 3.4e-06;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| |||||
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 25
US-09-863-600E-10
; Sequence 10, Application US/09863600E
; Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-09-863-600E-10

Query Match 72.4%; Score 89; DB 12; Length 20;
Best Local Similarity 68.4%; Pred. No. 8.8e-06;
Matches 13; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 GTASCHFGPLTWCKPQGG 20
| ||||| |||||
Db 2 GNYMCHFGPITWVCRPGG 20

RESULT 26
US-09-863-600E-44
; Sequence 44, Application US/09863600E
; Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia

; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 44
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-09-863-600E-44

Query Match 72.4%; Score 89; DB 12; Length 20;
Best Local Similarity 65.0%; Pred. No. 8.8e-06;
Matches 13; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| |||||
Db 1 GGLYACHMGPMTWVCPGG 20

RESULT 27
US-09-863-600E-24
; Sequence 24, Application US/09863600E
; Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-09-863-600E-24

Query Match 69.1%; Score 85; DB 12; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.3e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 SCHFGPLTWCKP 17
||||| |||||
Db 2 SCHFGPLTWCKP 14

RESULT 28
US-09-863-600E-9
; Sequence 9, Application US/09863600E
; Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael

; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-09-863-600E-9

Query Match 69.1%; Score 85; DB 12; Length 20;
Best Local Similarity 70.0%; Pred. No. 3.2e-05;
Matches 14; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
||| | ||||| |||
Db 1 GGDYHCRMGPLTWCKPLGG 20

RESULT 29
US-09-863-600E-45
; Sequence 45, Application US/09863600E
; Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-09-863-600E-45

Query Match 66.7%; Score 82; DB 12; Length 22;
Best Local Similarity 76.5%; Pred. No. 9.1e-05;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKP 17
| ||||| |||
Db 2 GRKYSCHFGPLTWVCQ 18

RESULT 30
US-09-863-600E-11
; Sequence 11, Application US/09863600E
; Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos

; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-09-863-600E-11

Query Match 65.9%; Score 81; DB 12; Length 20;
Best Local Similarity 60.0%; Pred. No. 0.00012;
Matches 12; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
||| | ||||| |||
Db 1 GGVYACRMGPITWVCSPLGG 20

RESULT 31
US-09-863-600E-14
; Sequence 14, Application US/09863600E
; Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-09-863-600E-14

Query Match 65.9%; Score 81; DB 12; Length 20;
Best Local Similarity 60.0%; Pred. No. 0.00012;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
||| | ||||| |||
Db 1 GGLYACHMGPMTWVCQLRG 20

RESULT 32
US-09-863-600E-18
; Sequence 18, Application US/09863600E
; Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda

; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-09-863-600E-18

Query Match 63.4%; Score 78; DB 12; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 SCHFGPLTWCK 16
| | | | | | | |
Db 1 SCHFGPLTWCK 12

RESULT 33
US-10-271-343-14
; Sequence 14, Application US/10271343
; Publication No. US2003016003A1
; GENERAL INFORMATION:
; APPLICANT: Cochran, Andrea G.
; APPLICANT: Skelton, Nicholas J.
; APPLICANT: Starevasnik, Melissa A.
; TITLE OF INVENTION: A STRUCTURED PEPTIDE SCAFFOLD FOR DISPLAYING TURN LIBRARIES
; FILE REFERENCE: 11669.116US11
; CURRENT APPLICATION NUMBER: US/10/271,343
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 09/592,695
; PRIOR FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: US 60/139,017
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Turn Peptide
US-10-271-343-14

Query Match 63.4%; Score 78; DB 12; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 SCHFGPLTWCK 16
| | | | | | | |
Db 1 SCHFGPLTWCK 12

RESULT 34
US-09-863-600E-16
; Sequence 16, Application US/09863600E
; Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis

; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-09-863-600E-16

Query Match 63.4%; Score 78; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 SCHFGPLTWCK 16
| | | | | | | |
Db 2 SCHFGPLTWCK 13

RESULT 35
US-10-006-593-3
; Sequence 3, Application US/10006593
; Publication No. US20030049683A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Renshaw, Mark
; TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
; FILE REFERENCE: 1087-2
; CURRENT APPLICATION NUMBER: US/10/006,593
; CURRENT FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/251,448
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: US 60/288,889
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/294,068
; PRIOR FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 18
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: EPO mimetic peptide
US-10-006-593-3

Query Match 62.6%; Score 77; DB 15; Length 18;
Best Local Similarity 80.0%; Pred. No. 0.00038;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 CHFGPLTWCKPQGG 20
| | | | | | | |
Db 4 CRMGPLTWCKPLGG 18

RESULT 36
US-09-863-600E-25
; Sequence 25, Application US/09863600E
; Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis

; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-09-863-600E-25

Query Match 59.3%; Score 73; DB 12; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 SCHFGPLTWVC 15
| | | | | | | | | |
Db 2 SCHFGPLTWVC 12

RESULT 37
US-09-863-600E-26
; Sequence 26, Application US/09863600E
; Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-09-863-600E-26

Query Match 56.9%; Score 70; DB 12; Length 13;
Best Local Similarity 91.7%; Pred. No. 0.0026;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 SCHFGPLTWVC 16
| | | | | | | | | |
Db 2 SCHFGPLTWVC 13

RESULT 38
US-09-863-600E-17
; Sequence 17, Application US/09863600E
; Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana

; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-09-863-600E-17

Query Match 56.1%; Score 69; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CHFGPLTWVC 15
| | | | | | | | | |
Db 2 CHFGPLTWVC 11

RESULT 39
US-09-863-600E-12
; Sequence 12, Application US/09863600E
; Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-09-863-600E-12

Query Match 55.3%; Score 68; DB 12; Length 19;
Best Local Similarity 55.6%; Pred. No. 0.0071;
Matches 10; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 GTASCHFGPLTWCKPQG 19
| | | | | | | | | |
Db 2 GNYMAHMGPIITWVCRPG 19

RESULT 40
US-09-863-600E-7
; Sequence 7, Application US/09863600E
; Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides

```

; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-09-863-600E-7

Query Match          53.7%; Score 56; DB 12; Length 20;
Best Local Similarity 55.0%; Pred. No. 0.314;
Matches 11; Conservative 2; Mismatches 7; Indels 7; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
   ||| ||| ||| |||
Db 1 GGLYLCRFGPVTWDCGYKGG 20

RESULT 41
US-10-006-593-71
; Sequence 71, Application US/10006593
; Publication No. US20030049683A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Renshaw, Mark
; TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
; FILE REFERENCE: 1087-2
; CURRENT APPLICATION NUMBER: US/10/006,593
; CURRENT FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/251,448
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: US 60/288,889
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/294,068
; PRIOR FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 71
; LENGTH: 22
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: EPO mimetic with random flanking amino acids
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(2)
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (6)..(6)
; OTHER INFORMATION: Xaa is any amino acid
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (15)..(15)
; OTHER INFORMATION: Xaa is any amino acid
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (21)..(22)
; OTHER INFORMATION: Xaa is any amino acid
US-10-006-593-71

Query Match          46.3%; Score 57; DB 15; Length 22;
Best Local Similarity 83.3%; Pred. No. 0.28;
Matches 10; Conservative 0; Mismatches 2; Indels 2; Gaps 0;

QY 9 GPLTWCKPQGG 20

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Db 9 GPLTWCKPLGG 20
||| ||| ||| |||

RESULT 42
US-09-863-600E-27
; Sequence 27, Application US/09863600E
; Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-09-863-600E-27

Query Match          43.9%; Score 54; DB 12; Length 14;
Best Local Similarity 55.0%; Pred. No. 0.48;
Matches 11; Conservative 1; Mismatches 2; Indels 6; Gaps 2;

QY 1 GGTASCHFGPLTWCKPQGG 20
   ||| ||| ||| |||
Db 1 GG---CRIGPITWVC---GG 14

RESULT 43
US-09-858-935B-43
; Sequence 43, Application US/09858935B
; Publication No. US20030069177A1
; GENERAL INFORMATION:
; APPLICANT: Dubaquitte, Yves
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Lowman, Henry B.
; TITLE OF INVENTION: METHOD FOR TREATING CARTILAGE DISORDERS
; FILE REFERENCE: P1794R1
; CURRENT APPLICATION NUMBER: US/09/858,935B
; CURRENT FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 60/248,985
; PRIOR FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: US 60/204,490
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 43
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-09-858-935B-43

Query Match          43.1%; Score 53; DB 11; Length 21;
Best Local Similarity 53.3%; Pred. No. 0.96;
Matches 8; Conservative 2; Mismatches 5; Indels 5; Gaps 0;

QY 2 GTASCHFGPLTWCK 16
   ||| ||| |||
Db 1 GQSCRAGPJQWLCE 15

```

RESULT 44
 US-09-863-600E-15
 ; Sequence 15, Application US/09863600E
 ; Publication No. US20030130197A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Smith-Swintosky, Virginia
 ; APPLICANT: Renzi, Michael
 ; APPLICANT: Plata-Salaman, Carlos
 ; APPLICANT: Jolliffe, Linda
 ; APPLICANT: Farrell, Francis
 ; APPLICANT: Johnson, Dana
 ; TITLE OF INVENTION: Neuroprotective Peptides
 ; FILE REFERENCE: PRI-0014 (ORT-1436)
 ; CURRENT APPLICATION NUMBER: US/09/863,600E
 ; CURRENT FILING DATE: 2001-05-23
 ; PRIOR APPLICATION NUMBER: 60/207,654
 ; PRIOR FILING DATE: 2000-05-26
 ; NUMBER OF SEQ ID NOS: 49
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 15
 ; LENGTH: 22
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic Peptide
 US-09-863-600E-15

Query Match 43.1%; Score 53; DB 12; Length 22;
 Best Local Similarity 58.3%; Pred. No. 1;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 6 CHFGPLTWVCKP 17
 Db 7 CYMGPEWECRP 18

RESULT 45
 US-09-863-600E-28
 ; Sequence 28, Application US/09863600E
 ; Publication No. US20030130197A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Smith-Swintosky, Virginia
 ; APPLICANT: Renzi, Michael
 ; APPLICANT: Plata-Salaman, Carlos
 ; APPLICANT: Jolliffe, Linda
 ; APPLICANT: Farrell, Francis
 ; APPLICANT: Johnson, Dana
 ; TITLE OF INVENTION: Neuroprotective Peptides
 ; FILE REFERENCE: PRI-0014 (ORT-1436)
 ; CURRENT APPLICATION NUMBER: US/09/863,600E
 ; CURRENT FILING DATE: 2001-05-23
 ; PRIOR APPLICATION NUMBER: 60/207,654
 ; PRIOR FILING DATE: 2000-05-26
 ; NUMBER OF SEQ ID NOS: 49
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 28
 ; LENGTH: 8
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic Peptide
 US-09-863-600E-28

Query Match 41.5%; Score 51; DB 12; Length 8;
 Best Local Similarity 100.0%; Pred. No. 5.8e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 HFGPLTWV 14
 Db 1 HFGPLTWV 8

RESULT 46
 US-09-858-935B-153
 ; Sequence 153, Application US/09858935B
 ; Publication No. US20030069177A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dubaquié, Yves
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Lowman, Henry B.
 ; TITLE OF INVENTION: METHOD FOR TREATING CARTILAGE DISORDERS
 ; FILE REFERENCE: P1794R1
 ; CURRENT APPLICATION NUMBER: US/09/858,935B
 ; CURRENT FILING DATE: 2002-07-02
 ; PRIOR APPLICATION NUMBER: US 60/248,985
 ; PRIOR FILING DATE: 2000-11-15
 ; PRIOR APPLICATION NUMBER: US 60/204,490
 ; PRIOR FILING DATE: 2000-05-16
 ; NUMBER OF SEQ ID NOS: 153
 ; SEQ ID NO 153
 ; LENGTH: 21
 ; TYPE: PRT
 ; ORGANISM: Artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: Sequence is synthesized
 US-09-858-935B-153

Query Match 41.5%; Score 51; DB 11; Length 21;
 Best Local Similarity 53.3%; Pred. No. 1.8;
 Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 2 GTASCHFGPLTWVCK 16
 Db 1 GQSCAAGPLQWLCE 15

RESULT 47
 US-09-858-935B-46
 ; Sequence 46, Application US/09858935B
 ; Publication No. US20030069177A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dubaquié, Yves
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Lowman, Henry B.
 ; TITLE OF INVENTION: METHOD FOR TREATING CARTILAGE DISORDERS
 ; FILE REFERENCE: P1794R1
 ; CURRENT APPLICATION NUMBER: US/09/858,935B
 ; CURRENT FILING DATE: 2002-07-02
 ; PRIOR APPLICATION NUMBER: US 60/248,985
 ; PRIOR FILING DATE: 2000-11-15
 ; PRIOR APPLICATION NUMBER: US 60/204,490
 ; PRIOR FILING DATE: 2000-05-16
 ; NUMBER OF SEQ ID NOS: 153
 ; SEQ ID NO 46
 ; LENGTH: 23
 ; TYPE: PRT
 ; ORGANISM: Artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: Sequence is synthesized
 US-09-858-935B-46

Query Match 41.5%; Score 51; DB 11; Length 23;
 Best Local Similarity 53.3%; Pred. No. 2;
 Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 2 GTASCHFGPLTWVCK 16
 Db 1 GQSCAAGPLQWLCE 15

RESULT 48
 US-09-858-935B-47
 ; Sequence 47, Application US/09858935B
 ; Publication No. US20030069177A1
 ; GENERAL INFORMATION:

APPLICANT: Dubaquitte, Yves
APPLICANT: Filvaroff, Ellen
APPLICANT: Lewman, Henry B.
TITLE OF INVENTION: METHOD FOR TREATING CARTILAGE DISORDERS
FILE REFERENCE: P1794R1
CURRENT APPLICATION NUMBER: US/09/858,935B
CURRENT FILING DATE: 2002-07-02
PRIOR APPLICATION NUMBER: US 60/248,985
PRIOR FILING DATE: 2000-11-15
PRIOR APPLICATION NUMBER: US 60/204,490
PRIOR FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 153
SEQ ID NO 47
LENGTH: 97
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Sequence is synthesized
US-09-858-935B-47

Query Match: 41.5%; Score 51; DB 1; Length 97;
Best Local Similarity 53.3%; Pred. No. 7.5;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 GTASCHFGPLTWCK 16
| | | | | | | | | |
DB : GQSCAAGPLQWLCE 15

RESULT 49
US-09-864-761-40377
Sequence 40377, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
SEQ ID NO 40377
LENGTH: 24
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AL132654.12
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.5
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.2
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.2
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.8
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.3
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.2
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.3
OTHER INFORMATION: EST_HUMAN HIT: A1208765.1, EVALUE 9.00e-08
US-09-864-761-40377

Query Match: 39.8%; Score 49; DB 9; Length 24;
Best Local Similarity 50.0%; Pred. No. 3.9;
Matches 10; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

QY 2 GTASC--HFGPLTWCKPQG 19
| | | | | | | | | | | | | | | |
DB 2 GTSSCTARRGPLAWRTSPRG 21

RESULT 50
US-09-864-761-48118
Sequence 48118, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 48118
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC010850.2
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.89
; OTHER INFORMATION: EST_HUMAN HIT: BF575401.1, EVALUE 5.40e+00
US-09-864-761-48118

Query Match 39.0%; Score 48; DB 9; Length 42;
Best Local Similarity 77.8%; Pred. NO. 9.1;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 10 PLTWCKPQ 18
Db 18 PLTWCSPR 26

Search completed: November 5, 2003, 19:12:07
Job time : 30 secs

GenCore version 5.1.6
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OX protein - protein search, using sw model

Run on: November 5, 2003, 19:03:58 ; Search time 21 Seconds
(without alignments)
91.589 Million cell updates/sec

Title: US-09-863-600E-19
Perfect score: 123
Sequence: 1 GGTASCHFGPLTWCKPQGG 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	58	47.2	19	1 EWSMAN	ancovenin - Strept
2	50.5	41.1	155	2 C69002	conserved hypother
3	50	40.7	19	1 EWSMCN	cinnamycin - Strep
4	50	40.7	78	1 EWSMYG	cinnamycin precurs
5	49	39.8	499	2 S63465	dihydroliipoamide d
6	47	38.2	68	2 S36976	hypothetical prote
7	47	38.2	319	2 T47852	hypothetical prote
8	47	38.2	640	2 T29784	hypothetical prote
9	47	38.2	695	2 T52429	PRM1 homolog limpo
10	46	37.4	240	2 S34619	probable fumarate
11	46	37.4	272	2 AI2005	delta-9 desaturase
12	46	37.4	347	2 T33018	hypothetical prote
13	45.5	37.0	498	1 HJBE11	helicase (EC 3.6.1
14	45	36.6	126	2 S54062	hypothetical prote
15	45	36.6	220	2 AI2182	hypothetical prote
16	45	36.6	346	2 S34732	membrane protein -
17	45	36.6	370	2 C75268	carboxypeptidase G
18	45	36.6	1290	2 AE2192	two-component hybr
19	45	36.6	1622	2 D86428	glutathione S-conj
20	45	36.6	2910	2 T28156	DNA-directed RNA p
21	44	35.8	314	2 T17764	hypothetical prote
22	44	35.8	338	2 T49229	palmitoyl-protein
23	44	35.8	387	2 S46123	hypothetical prote
24	44	35.8	388	2 A83913	xylanase Y BH2105
25	44	35.8	522	1 KJHUG6	N-acetylgalactosam
26	44	35.8	733	2 A97415	hypothetical prote
27	44	35.8	735	2 G02937	fertilin beta - cr
28	44	35.8	1539	2 S65775	homeotic protein H
29	43.5	35.4	437	2 S39069	vasoactive intesti

30	43	35.0	119	2	B98236	exsl protein prote
31	43	35.0	123	2	S29714	guanine-nucleotide
32	43	35.0	123	2	I52427	guanine-nucleotide
33	43	35.0	199	2	A46711	probable thioredox
34	43	35.0	356	2	T22998	hypothetical prote
35	43	35.0	397	2	T30088	hypothetical prote
36	43	35.0	483	2	A38560	nitrate transport
37	43	35.0	626	2	H82133	conserved hypother
38	43	35.0	1520	2	T00273	hypothetical prote
39	42.5	34.6	96	2	E69273	hypothetical prote
40	42.5	34.6	347	2	S50403	TIF34 protein - ye
41	42	34.1	165	2	D84394	hypothetical prote
42	42	34.1	199	2	A48513	macrophage 23K str
43	42	34.1	199	2	I52425	probable thioredox
44	42	34.1	288	2	B59405	prolactin receptor
45	42	34.1	347	2	T41373	hypothetical prote
46	42	34.1	376	2	A59405	prolactin receptor
47	42	34.1	426	2	A35641	5-aminimidazole r
48	42	34.1	554	2	E87375	conserved hypother
49	42	34.1	622	2	A40144	prolactin receptor
50	42	34.1	679	2	T00636	hypothetical prote
51	42	34.1	872	2	H86435	protein F17F8.5 [l
52	42	34.1	902	2	AD0587	sensor protein Kdp
53	42	34.1	1506	2	T30886	integumentary muc
54	41.5	33.7	60	2	A82662	hypothetical prote
55	41.5	33.7	155	2	C64314	conserved hypother
56	41.5	33.7	342	2	JT0370	hypothetical prote
57	41.5	33.7	982	1	GNLJH2	pol polyprotein -
58	41.5	33.7	1133	1	GNVUSR	M polyprotein prec
59	41.5	33.7	1133	1	A43964	M polyprotein prec
60	41.5	33.7	1133	2	S12597	M polyprotein prec
61	41.5	33.7	1134	1	GNVU22	M polyprotein prec
62	41.5	33.7	1134	1	A43960	M polyprotein prec
63	41	33.3	128	2	T06028	hypothetical prote
64	41	33.3	197	2	A69201	rubrerythrin - Met
65	41	33.3	229	2	C71493	probable uracil DN
66	41	33.3	229	2	B81652	uracil-DNA glycosy
67	41	33.3	239	2	C81935	probable ribonucle
68	41	33.3	239	2	E81169	ribonuclease III N
69	41	33.3	248	2	D64242	sporulation protei
70	41	33.3	306	2	AB2685	conserved hypother
71	41	33.3	306	2	G97466	diheme cytochrome
72	41	33.3	330	2	A40855	homeotic protein H
73	41	33.3	338	2	D89102	protein F25E5.2 [l
74	41	33.3	347	2	T20472	hypothetical prote
75	41	33.3	405	4	A61181	homeotic protein H
76	41	33.3	471	1	KHRZOB	oryzain (EC 3.4.22
77	41	33.3	473	2	I49283	ADAM 4 protein pre
78	41	33.3	608	2	F83397	probable peptidase
79	41	33.3	650	2	B87466	TonB-dependent rec
80	41	33.3	756	2	G86150	F22M8.3 protein -
81	41	33.3	814	2	G02390	disintegrin-like m
82	41	33.3	873	1	I48952	VLDL receptor prec
83	41	33.3	906	2	G96621	probable disease r
84	40.5	32.9	290	2	F90154	SSV1 integrase hom
85	40.5	32.9	300	2	T52020	ethylene responsiv
86	40.5	32.9	437	2	JU0185	PACAP/vip receptor
87	40.5	32.9	566	1	HM1VDU	hemagglutinin prec
88	40.5	32.9	1142	1	GNVUPH	M polyprotein prec
89	40.5	32.9	1225	2	T09395	envelope polyprote
90	40	32.5	71	1	I40863	piscicollin 61 prec
91	40	32.5	103	2	B72003	hypothetical prote
92	40	32.5	103	2	H86621	hypothetical prote
93	40	32.5	144	2	G86809	transcription regu
94	40	32.5	147	2	E82523	hypothetical prote
95	40	32.5	158	2	B82191	hypothetical prote
96	40	32.5	212	2	E64123	stringent starvati
97	40	32.5	244	2	T44604	beta-lactamase-lik
98	40	32.5	255	2	A71351	probable cobalt AB
99	40	32.5	316	2	D90585	hypothetical prote
100	40	32.5	331	2	D88986	protein C50H11.12

ALIGNMENTS

```
RESULT 1
EWSMAN
ancovenin - Streptomyces sp. (strain A647P-2)
C:Species: Streptomyces sp.
C>Date: 12-May-1994 #sequence_revision 19-May-1994 #text_change 19-May-1994
C:Accession: A61284
R;Wakamiya, T.; Ueki, Y.; Shiba, T.; Kido, Y.; Motoki, Y.
Tetraedron Lett. 26, 665-668, 1985
A:Title: The structure of ancovenin, a new peptide inhibitor of angiotensin I converting
A:Reference number: A61284
A:Accession: A61284
A:Molecule type: protein
A:Residues: 1-19 <WAK>
C:Superfamily: cinnamycin precursor
C:Keywords: antibiotic; lanthionine
F:1-18/Cross-link: (2S,3S,6R)-3-methyl-lanthionine (Cys-Thr) #status experimental
F:1-14/Cross-link: sn-(2S,6R)-lanthionine (Ser-Cys) #status experimental
F:5-11/Cross-link: (2S,3S,6R)-3-methyl-lanthionine (Cys-Thr) #status experimental
F:6/Modified site: dehydroalanine (Ser) #status experimental

Query Match 47.2%; Score 58; DB 1; Length 19;
Best Local Similarity 81.8%; Pred. No. 0.045;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 SCHFGPLTWVC 15
Db 4 SCSFGPLTWSC 14

RESULT 2
C69002
conserved hypothetical protein MTH1014 - Methanobacterium thermoautotrophicum (strain De
N;Alternate names: orf2 atWA 3'-region
C:Species: Methanobacterium thermoautotrophicum
C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 08-Oct-1999
C:Accession: C69002; C36921
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiواني, N.
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A:Reference number: A69000; MUID:98037514; PMID:9371463
A:Accession: C69002
A>Status: nucleic acid sequence not shown; translation not shown;
A:Molecule type: DNA
A:Residues: 1-155 <MTH>
A:Cross-references: GB:AE000874; GB:AE000666; NID:g2622110; PIDN:AAB85510.1; PID:g262211
A:Experimental source: strain Delta H
R;Kuhner, C.H.; Linderbach, B.D.; Wolfe, R.S.
J. Bacteriol. 175, 3195-3203, 1993
A:Title: Component A2 of methylcoenzyme M reductase system from Methanobacterium thermoa
A:Reference number: A36921; MUID:93259970; PMID:8491734
A:Accession: C36921
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 32-66 <KUH>
A:Cross-references: GB:S61233; NID:g385922; PIDN:AAB26632.1; PID:g385925
A:Experimental source: strain Delta H
A:Note: sequence extracted from NCBI backbone (NCBIN:132019, NCBIP:132022)
C:Genetics:
A:Gene: MTH1014
A:Start codon: TTG
C:Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0115

Query Match 41.1%; Score 50.5; DB 2; Length 155;
Best Local Similarity 56.2%; Pred. No. 3.7;
Matches 9; Conservative 1; Mismatches 5; Indels 1; Gaps 1;

QY 2 GTASCHFGPLTWCKP 17
; : | | | | | | |
```

Db 61 GQGTC-FGSLVMCKP 75

```
RESULT 3
EWSMCN
cinnamycin - Streptovorticillium cinnamoneum
N;Alternate names: lanthiopeptin; lantibiotic Ro 09-0198
C:Species: Streptovorticillium cinnamoneum
C>Date: 30-Sep-1993 #sequence_revision 12-May-1994 #text_change 07-May-1999
C:Accession: A45767
R;Naruse, N.; Tenmyo, O.; Tomita, K.; Konishi, M.; Miyaki, T.; Kawaguchi, H.; Fukase,
J. Antibiot. 42, 837-845, 1989
A:Title: Lanthiopeptin, a new peptide antibiotic. Production, isolation and propertie
A:Reference number: A45767; MUID:89291558; PMID:2544544
A:Accession: A45767
A:Molecule type: protein
A:Residues: 1-19 <NAR>
R;Wakamiya, T.; Fukase, K.; Naruse, N.; Konishi, M.; Shiba, T.
Tetraedron Lett. 29, 4771-4772, 1988
A:Title: Lanthiopeptin, a new peptide effective against Herpes simplex virus: structu
A:Reference number: A53359
A:Contents: annotation; strain L337-2
C:Superfamily: cinnamycin precursor
C:Keywords: antibiotic; beta-hydroxyaspartic acid; lanthionine
F:1-18/Cross-link: (2S,3S,6R)-3-methyl-lanthionine (Cys-Thr) #status experimental
F:4-14/Cross-link: sn-(2S,6R)-lanthionine (Ser-Cys) #status experimental
F:5-11/Cross-link: (2S,3S,6R)-3-methyl-lanthionine (Cys-Thr) #status experimental
F:6-19/Cross-link: (2Xi,9S)-lysinoalanine (Ser-Lys) #status experimental
F:15/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental

Query Match 40.7%; Score 50; DB 1; Length 19;
Best Local Similarity 72.7%; Pred. No. 0.65;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 SCHFGPLTWVC 15
Db 4 SCSFGPFTFVC 14

RESULT 4
EWSMYG
cinnamycin precursor - Streptovorticillium griseovorticillatum
N;Alternate names: lanthiopeptin; lantibiotic Ro 09-0198
C:Species: Streptovorticillium griseovorticillatum
C>Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 18-Jun-1999
C:Accession: S17181; A60555
R;Kalletta, C.; Entian, K.D.; Jung, G.
Eur. J. Biochem. 199, 411-415, 1991
A:Title: Peptide sequence of cinnamycin (Ro 09-0198): the first structural gene of
A:Reference number: S17181; MUID:91301152; PMID:2070795
A:Accession: S17181
A:Molecule type: DNA
A:Residues: 1-78 <KAL>
A:Cross-references: EMBL:X58545; NID:g47089; PIDN:CAA41436.1; PID:g47090
R;Kessler, H.; Steuernagel, S.; Will, M.; Jung, G.; Kellner, R.; Gillesen, D.; Kamiy
Helv. Chim. Acta 71, 1924-1929, 1988
A:Title: The structure of the polycyclic nonadecapeptide Ro 09-0198.
A:Reference number: A60555
A:Accession: A60555
A:Molecule type: protein
A:Residues: 60-78 <KES>
C:Genetics:
A:Gene: cinA; rocA
C:Superfamily: cinnamycin precursor
C:Keywords: antibiotic; beta-hydroxyaspartic acid; lanthionine
F:1-59/Domain: propeptide #status predicted <PRO>
F:60-78/Product: cinnamycin #status experimental <MAT>
F:60-77/Cross-link: (2S,3S,6R)-3-methyl-lanthionine (Cys-Thr) #status experimental
F:63-73/Cross-link: sn-(2S,6R)-lanthionine (Ser-Cys) #status experimental
F:64-70/Cross-link: (2S,3S,6R)-3-methyl-lanthionine (Cys-Thr) #status experimental
F:65-78/Cross-link: (2Xi,9S)-lysinoalanine (Ser-Lys) #status experimental
F:74/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
```



```
Matches      8;  Conservative      0;  Mismatches      8;  Indels      0;  Gaps      0;

QY      3  TASCHFGPLTWCKPQ 18
      ||| ||| |||
Db      185 TVKSHFAQLAWCVSQ 200

RESULT 10
S34619
probable fumarate reductase (EC 1.3.99.1) iron-sulfur protein - Thermoplasma acidophilum
C:Species: Thermoplasma acidophilum
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 11-Jun-1999
C:Accession: S34619
R:Baeh, M.; Reilaender, H.; Gaertner, P.; Lottspeich, F.; Michel, H.
Biochim. Biophys. Acta 1174, 103-107, 1993
A:Title: Nucleotide sequence of a putative succinate dehydrogenase operon in Thermoplasma
A:Reference number: S34619; MUID:93326626; PMID:8334158
A:Accession: S34619
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-240 <BAC>
A:Cross-references: EMBL:X70908; NID:g396211; PIDN:CAA50262.1; PID:g396212
C:Superfamily: fumarate reductase iron-sulfur protein; ferredoxin 2[4Fe-4S] homology; ferredoxin
C:Keywords: 2Fe-2S; 3Fe-4S; 4Fe-4S; iron-sulfur protein; metalloprotein; oxidoreductase
F:33-75/Domain: ferredoxin [2Fe-2S] homology <FER1>
F:139-220/Domain: ferredoxin 2[4Fe-4S] homology <FER2>
F:54,59,62,74/Binding site: 2Fe-2S cluster (Cys) (covalent) #status predicted
F:146,149,152,212/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted
F:156,202,208/Binding site: 3Fe-4S cluster (Cys) (covalent) #status predicted

      Query Match      37.4%; Score 46; DB 2; Length 240;
      Best Local Similarity 57.9%; Pred. No. 25;
      Matches 11; Conservative 2; Mismatches 4; Indels 2; Gaps 2;

QY      2  GTASCHF-GPLTWCKPQ 19
      ||| ||| ||| |||
Db      198 GTSRCHFAGECTEVC-PKG 215

RESULT 11
AI2005
delta-9 desaturase [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C:Accession: AI2005
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A:Reference number: AB1807; MUID:21595285; PMID:11759940
A:Accession: AI2005
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-272 <KUR>
A:Cross-references: GB:BA000019; PIDN:BA077965.1; PID:g17135419; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: desc
C:Superfamily: mammalian stearyl-CoA desaturase; stearyl-CoA desaturase homology

      Query Match      37.4%; Score 46; DB 2; Length 272;
      Best Local Similarity 53.8%; Pred. No. 28;
      Matches 7; Conservative 2; Mismatches 4; Indels 4; Gaps 0;

QY      2  GTASCHFGPLTW 14
      ||| ||| |||
Db      82 GTLACQGPIEW 94

RESULT 12
T33018
hypothetical protein K07H8.8 - Caenorhabditis elegans
```

```
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C:Accession: T33018
R:Fulton, B.; Hawkins, J.; Gattung, S.; Wohldmann, P.; Elliott, G.
submitted to the EMBL Data Library, February 1998
A:Description: The sequence of C. elegans cosmid K07H8.
A:Reference number: Z21264
A:Accession: T33018
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-347 <FUL>
A:Cross-references: EMBL:AF047659; PIDN:AAC04429.1; GSPDB:GN00022; CESP:K07H8.8
A:Experimental source: strain Bristol N2; clone K07H8
C:Genetics:
A:Gene: CESP:K07H8.8
A:Map position: 4
A:Introns: 47/1; 110/3; 158/2; 202/2; 249/2; 302/1

      Query Match      37.4%; Score 46; DB 2; Length 347;
      Best Local Similarity 58.3%; Pred. No. 35;
      Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      4  ASCHFGPLTWVC 15
      ||| ||| |||
Db      240 ADTHFAPQTWYC 251

RESULT 13
HJBH11
helicase (EC 3.6.1.-) - ictalurid herpesvirus 1 (strain auburn 1)
C:Species: ictalurid herpesvirus 1
A:Note: host Ictalurus punctatus (channel catfish)
C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 19-Jan-2001
C:Accession: H36788
R:Davidson, A.J.
submitted to GenBank, January 1992
A:Description: Channel catfish virus: a new type of herpesvirus.
A:Reference number: A36804
A:Accession: H36788
A:Molecule type: DNA
A:Residues: 1-498 <DAV>
A:Cross-references: GB:M75136; NID:g331209; PIDN:AAA88128.1; PID:g331235
R:Davidson, A.J.
Virology 186, 9-14, 1992
A:Title: Channel catfish virus: a new type of herpesvirus.
A:Reference number: A39447; MUID:92087490; PMID:1727613
A:Contents: annotation
A:Note: neither amino acid nor nucleotide sequence is given
C:Genetics:
A:Gene: 25
C:Superfamily: ictalurid herpesvirus helicase
C:Keywords: ATP; DNA binding; DNA repair; DNA replication; hydrolase; nucleotide bin
F:37-44/Region: nucleotide-binding motif A (P-loop)

      Query Match      37.0%; Score 45.5; DB 1; Length 498;
      Best Local Similarity 56.2%; Pred. No. 57;
      Matches 9; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

QY      1  GGTASCHFGPL-TWVC 15
      ||| ||| ||| |||
Db      323 GGSASCRFGALIEYMC 338

RESULT 14
S54062
hypothetical protein YML122c - Yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein YM7056.04c
C:Species: Saccharomyces cerevisiae
C:Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 19-Apr-2002
C:Accession: S54062
R:Badcock, K.; Churcher, C.M.
submitted to the EMBL Data Library, May 1995
A:Reference number: S54059
```

A;Accession: S54062
A;Molecule type: DNA
A;Residues: 1-126 <BAD>
A;Cross-references: EMBL:249218; NID:g805016; PIDN:CAA89158.1; PID:g805020; GSPDB:GN0001
A;Experimental source: strain AB972
C;Genetics:
A;Gene: MIPS:YML122C
A;Cross-references: SGD:S0004591
A;Map position: 13L
C;Superfamily: Saccharomyces hypothetical protein YML122c

Query Match 36.6%; Score 45; DB 2; Length 126;
Best Local Similarity 53.8%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 TASCHFGPLTWVC 15
||| | |||
Db 53 TARCQFNSSTWTC 65

RESULT 15
A12182
hypothetical protein all3016 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: A12182
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: A12182
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-220 <KUR>
A;Cross-references: GB:BA000019; PIDN:BA074715.1; PID:gl7132110; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: all3016

Query Match 36.6%; Score 45; DB 2; Length 220;
Best Local Similarity 61.5%; Pred. No. 32;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 8 FGPLTWCKPQGG 20
| : |||||
Db 131 FAEIKRVCKPQGG 143

RESULT 16
S34732
membrane protein - Bacillus acidopullulyticus
C;Species: Bacillus acidopullulyticus
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 15-Oct-1999
C;Accession: S34732
R;Kelly, A.P.; Diderichsen, B.; Jorgensen, S.T.; McConnell, D.J.
submitted to the EMBL Data Library, April 1993
A;Description: Molecular genetics analysis of a maltogenic amylase gene of Bacillus acid
A;Reference number: S34731
A;Accession: S34732
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-346 <XEL>
A;Cross-references: EMBL:Z22520; NID:g396082; PIDN:CAA80248.1; PID:g396084
C;Keywords: transmembrane protein

Query Match 36.6%; Score 45; DB 2; Length 346;
Best Local Similarity 77.8%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 CHFGPLTWV 14
| |||||

Db 319 CKFGPLEWV 327

RESULT 17
C75268
carboxypeptidase G2 - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 18-Aug-2000
C;Accession: C75268
R;White, O.; Eisen, J.A.; Heideberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.;
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: C75268
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-370 <WHI>
A;Cross-references: GB:AE002078; GB:AE000513; NID:g6460306; PIDN:AAF12031.1; PID:g646
A;Experimental source: strain R1
C;Genetics:
A;Gene: DR2493
A;Map position: 1
C;Superfamily: folate hydrolase G

Query Match 36.6%; Score 45; DB 2; Length 370;
Best Local Similarity 80.0%; Pred. No. 51;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGTASCHFGP 10
||| | |||
Db 58 GGTRSFHFGP 67

RESULT 18
AE2192
two-component hybrid sensor and regulator alr3092 [imported] - Nostoc sp. (strain PCC
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AE2192
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AE2192
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1290 <KUR>
A;Cross-references: GB:BA000019; PIDN:BA074791.1; PID:gl7132186; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: alr3092

Query Match 36.6%; Score 45; DB 2; Length 1290;
Best Local Similarity 57.1%; Pred. No. 1.6e+02;
Matches 8; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 GTASCHFGPLTWVC 15
| | |||||
Db 747 GAARLSSSPLTWVC 760

RESULT 19
D86428
glutathione S-conjugate transporting ATPase (AtMRP1) - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 27-Nov-2001
C;Accession: D86428
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,

ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, X.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: D86428
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1622 <STO>
A;Cross-references: GB:AE005172; NID:g11055814; PIDN:AAG28284.1; GSPDB:GN00141
C;Genetics:
A;Map position: 1
C;Superfamily: human multidrug resistance protein cMOAT2; ATP-binding cassette homology

Query Match 36.6%; Score 45; DB 2; Length 1622;
Best Local Similarity 70.0%; Pred. No. 2e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 8 FGPLTWVCKP 17
| | | | |
Db 3 FEPLDWYCKP 12

RESULT 20
T28156
DNA-directed RNA polymerase homolog - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000
C;Accession: T28156
R;Fox, B.A.; Li, W.B.; Tanaka, M.; Inselburg, J.; Bzik, D.J.
Mol. Biochem. Parasitol. 61, 37-48, 1993
A;Title: Molecular characterization of the largest subunit of plasmodium falciparum RNA
A;Reference number: Z20478; MUID:94081864; PMID:8259131
A;Accession: T28156
A;Status: preliminary; translated from GB/EMBL/CDSJ
A;Molecule type: DNA
A;Residues: 1-2910 <FOX>
A;Cross-references: EMBL:L11172; NID:g414321; PID:g414322; PIDN:AAA72349.1
C;Genetics:
A;Introns: 2840/3; 2880/1

Query Match 36.6%; Score 45; DB 2; Length 2910;
Best Local Similarity 60.0%; Pred. No. 3e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 7 HFGPLTWVCK 16
| | | | |
Db 2702 HFSPVTWILK 2711

RESULT 21
T17764
hypothetical protein A267L - Chlorella virus PCV-1
C;Species: Chlorella virus PCV-1
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T17764
R;Graves, M.V.; Van Eeten, J.L.
submitted to the EMBL Data Library, May 1999
A;Reference number: Z18806
A;Accession: T17764
A;Status: preliminary; translated from GB/EMBL/CDSJ
A;Molecule type: DNA
A;Residues: 1-314 <GRA>
A;Cross-references: EMBL:U42580; NID:g4028896; PIDN:AAC96635.1
A;Experimental source: specific host Chlorella strain NC64A
C;Genetics:
A;Note: A267L

Query Match 35.8%; Score 44; DB 2; Length 314;

Best Local Similarity 53.8%; Pred. No. 62;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTW 13
| | | | |
Db 188 GECAYCHRAPITW 200

RESULT 22
T49229
palmitoyl-protein thioesterase-like protein F27H5.130 [imported] - Arabidopsis thalia
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Sep-2000
C;Accession: T49229
R;Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Rudd, S.; Lemcke
submitted to the Protein Sequence Database, April 2000
A;Reference number: Z25018
A;Accession: T49229
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-338 <RIE>
A;Cross-references: EMBL:AL163852; GSPDB:GN00061; ATSP:F27H5.130
A;Experimental source: cultivar Columbia; BAC clone F27H5
C;Genetics:
A;Gene: ATSP:F27H5.130
A;Map position: 3
A;Introns: 30/1; 58/2; 75/3; 82/3; 117/3; 138/3; 160/3; 173/3; 213/3; 244/3

Query Match 35.8%; Score 44; DB 2; Length 338;
Best Local Similarity 57.1%; Pred. No. 66;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 2 GTASCHFGPLTWVC 15
| | | | |
Db 130 GTASIFCGATWIC 143

RESULT 23
S46123
hypothetical protein YBR246w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein YBR1634
C;Species: Saccharomyces cerevisiae
C;Date: 26-Aug-1994 #sequence_revision 09-Sep-1994 #text_change 19-Apr-2002
C;Accession: S46123
R;Aljinovic, G.; Pohl, F.M.; Pohl, T.M.
submitted to the Protein Sequence Database, August 1994
A;Reference number: S45906
A;Accession: S46123
A;Molecule type: DNA
A;Residues: 1-387 <ALJ>
A;Cross-references: EMBL:Z36115; NID:g536658; PID:g536659; GSPDB:GN00002; MIPS:YBR246
A;Experimental source: strain S288C
C;Genetics:
A;Gene: MIPS:YBR246w
A;Cross-references: SGD:S0000450
A;Map position: 2R

Query Match 35.8%; Score 44; DB 2; Length 387;
Best Local Similarity 69.2%; Pred. No. 75;
Matches 9; Conservative 0; Mismatches 2; Indels 2; Gaps 1;

Qy 4 ASCHFGPLTWCK 16
| | | | |
Db 125 ASCHFSPLD--CK 135

RESULT 24
AB3913
xylanase Y BH2105 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: AB3913
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; P

Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: A83913
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-388 <STO>
A;Cross-references: GB:AP001514; GB:BA000004; NID:g10174613; PIDN:BA05824.1; GSPDB:GN00
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH2105

Query Match 35.8%; Score 44; DB 2; Length 388;
Best Local Similarity 41.2%; Pred. No. 75;
Matches 7; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 3 TASCHFGPLTWCKPQ 19
Db 102 TEGVHAGYFAWSCQPDG 118

RESULT 25
KJHUG6
N-acetyl-galactosamine-6-sulfatase (EC 3.1.1.6.4) precursor [validated] - human
N;Alternate names: chondroitinase; chondroitinsulfatase; galactose-6-sulfate sulfatase;
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence revision 27-Oct-1995 #text_change 08-Dec-2000
C;Accession: JQ1299; PQ0242; I37406
R;Tomatsu, S.; Fukuda, S.; Masue, M.; Sukegawa, K.; Fukao, T.; Yamagishi, A.; Hori, T.;
ashi, Y.; Orii, T.
Biochem. Biophys. Res. Commun. 181, 677-683, 1991
A;Title: Morquio disease: isolation, characterization and expression of full-length cDNA
A;Reference number: JQ1299; MUID:92095973; PMID:1755850
A;Accession: JQ1299
A;Molecule type: mRNA
A;Residues: 1-522 <TOM>
A;Experimental source: placenta
A;Accession: PQ0242
A;Molecule type: protein
A;Residues: 27-42, 'X', 44-54; 175-183, 'X', 185-192; 201-218; 243-265; 311-324, 'XX', 327-336; 374
R;Morris, C.F.; Guo, X.H.; Apostolou, S.; Hopwood, J.J.; Scott, H.S.
Genomics 22, 652-654, 1994
A;Title: Morquio A syndrome: cloning, sequence, and structure of the human N-acetyl-galac
A;Reference number: I37406; MUID:95095267; PMID:8001980
A;Accession: I37406
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-522 <RES>
A;Cross-references: EMBL:U06088; NID:g507365; PIDN:AACS1350.1; PID:g618426
A;Note: nucleotide sequence not complete
C;Genetics:
A;Gene: GDB:GALNS
A;Cross-references: GDB:129085; OMIM:253000
A;Map position: 16q24-16q24
A;Introns: 40/3; 82/1; 107/1; 141/2; 189/2; 211/3; 253/2; 300/1; 334/3; 380/2; 414/3; 45
A;Note: defects in this gene can cause mucopolysaccharidosis type IV A, Morquio disease
C;Function:
A;Description: hydrolyzes N-acetyl-galactosamine-6-sulfate units in chondroitin sulfate a
C;Superfamily: animal sulfatase
C;Keywords: glycoprotein; sulfuric ester hydrolase
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-522/Product: N-acetyl-galactosamine-6-sulfatase #status experimental <MAT>
F;79/Modified site: 3-oxoalanine (Cys) #status predicted
F;204,423/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 35.8%; Score 44; DB 1; Length 522;
Best Local Similarity 43.8%; Pred. No. 98;
Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 2 GTASCHFGPLTWCKP 17
Db 16: GSPNCHFGPYDNKARP 176

Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: A83913
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-388 <STO>
A;Cross-references: GB:AP001514; GB:BA000004; NID:g10174613; PIDN:BA05824.1; GSPDB:GN00
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH2105

Query Match 35.8%; Score 44; DB 2; Length 388;
Best Local Similarity 41.2%; Pred. No. 75;
Matches 7; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 3 TASCHFGPLTWCKPQ 19
Db 102 TEGVHAGYFAWSCQPDG 118

RESULT 25
KJHUG6
N-acetyl-galactosamine-6-sulfatase (EC 3.1.1.6.4) precursor [validated] - human
N;Alternate names: chondroitinase; chondroitinsulfatase; galactose-6-sulfate sulfatase;
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence revision 27-Oct-1995 #text_change 08-Dec-2000
C;Accession: JQ1299; PQ0242; I37406
R;Tomatsu, S.; Fukuda, S.; Masue, M.; Sukegawa, K.; Fukao, T.; Yamagishi, A.; Hori, T.;
ashi, Y.; Orii, T.
Biochem. Biophys. Res. Commun. 181, 677-683, 1991
A;Title: Morquio disease: isolation, characterization and expression of full-length cDNA
A;Reference number: JQ1299; MUID:92095973; PMID:1755850
A;Accession: JQ1299
A;Molecule type: mRNA
A;Residues: 1-522 <TOM>
A;Experimental source: placenta
A;Accession: PQ0242
A;Molecule type: protein
A;Residues: 27-42, 'X', 44-54; 175-183, 'X', 185-192; 201-218; 243-265; 311-324, 'XX', 327-336; 374
R;Morris, C.F.; Guo, X.H.; Apostolou, S.; Hopwood, J.J.; Scott, H.S.
Genomics 22, 652-654, 1994
A;Title: Morquio A syndrome: cloning, sequence, and structure of the human N-acetyl-galac
A;Reference number: I37406; MUID:95095267; PMID:8001980
A;Accession: I37406
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-522 <RES>
A;Cross-references: EMBL:U06088; NID:g507365; PIDN:AACS1350.1; PID:g618426
A;Note: nucleotide sequence not complete
C;Genetics:
A;Gene: GDB:GALNS
A;Cross-references: GDB:129085; OMIM:253000
A;Map position: 16q24-16q24
A;Introns: 40/3; 82/1; 107/1; 141/2; 189/2; 211/3; 253/2; 300/1; 334/3; 380/2; 414/3; 45
A;Note: defects in this gene can cause mucopolysaccharidosis type IV A, Morquio disease
C;Function:
A;Description: hydrolyzes N-acetyl-galactosamine-6-sulfate units in chondroitin sulfate a
C;Superfamily: animal sulfatase
C;Keywords: glycoprotein; sulfuric ester hydrolase
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-522/Product: N-acetyl-galactosamine-6-sulfatase #status experimental <MAT>
F;79/Modified site: 3-oxoalanine (Cys) #status predicted
F;204,423/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 35.8%; Score 44; DB 1; Length 522;
Best Local Similarity 43.8%; Pred. No. 98;
Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 2 GTASCHFGPLTWCKP 17
Db 16: GSPNCHFGPYDNKARP 176

RESULT 26
A97415
hypothetical protein AGR_C_812 [imported] - *Agrobacterium tumefaciens* (strain C58, Ce
C;Species: *Agrobacterium tumefaciens*
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
C;Accession: A97415
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldm
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz,
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent *Agrobacterium*
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: A97415
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-733 <KUR>
A;Cross-references: GB:AE007869; PIDN:AAK86274.1; PID:g15155384; GSPDB:GN00169
C;Genetics:
A;Gene: AGR_C_812
A;Map position: circular chromosome

Query Match 35.8%; Score 44; DB 2; Length 733;
Best Local Similarity 46.2%; Pred. No. 1.3e+02;
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 8 FGPLTWCKPQGG 20
Db 348 YGPTQWACENQAG 360

RESULT 27
G02937
fertilin beta - crab-eating macaque
C;Species: *Macaca fascicularis* (crab-eating macaque)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 01-Dec-2000
C;Accession: G02937; S55061
R;Ramrao, C.S.; Myles, D.G.; White, J.M.; Primakoff, P.
submitted to the EMBL Data Library, August 1995
A;Reference number: G12615
A;Accession: G02937
A;Status: preliminary; translated from GB/EMBL/DBRJ
A;Molecule type: mRNA
A;Residues: 1-735 <RAM>
A;Cross-references: EMBL:U33959; NID:g998339; PID:g998340
R;Perry, A.C.F.; Gichuhi, P.M.; Jones, R.; Hall, L.
Biochem. J. 307, 843-850, 1995
A;Title: Cloning and analysis of monkey fertilin reveals novel alpha subunit isoforms
A;Reference number: S55059; MUID:95260313; PMID:7741716
A;Accession: S55061
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-722, 'S', 724-735 <PER>
A;Cross-references: EMBL:X77653; NID:g794076; PIDN:CAA54733.1; PID:g794077
C;Superfamily: mouse meltrin alpha; disintegrin homology
F;383-468/Domain: disintegrin homology <DIS>

Query Match 35.8%; Score 44; DB 2; Length 735;
Best Local Similarity 44.0%; Pred. No. 1.3e+02;
Matches 11; Conservative 1; Mismatches 3; Indels 10; Gaps 2;

QY 1 GGTASC---HF-----GPLTWVC 15
Db 460 GTSASCPENHFQTGHPCGPNQWVC 484

RESULT 28
S65775
homeotic protein Hox2b - maize
C;Species: *Zea mays* (maize)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 11-Jan-2002
C;Accession: S65775; S72455
R;Klinge, B.; Ueberlacker, B.; Korfhage, C.; Werr, W.
Plant Mol. Biol. 30, 439-453, 1996

Query Match 35.8%; Score 44; DB 1; Length 522;
Best Local Similarity 43.8%; Pred. No. 98;
Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 2 GTASCHFGPLTWCKP 17
Db 16: GSPNCHFGPYDNKARP 176

```
A;Title: ZmHox: a novel class of maize homeobox genes.
A;Reference number: S65774; MUID:96189260; PMID:8605297
A;Accession: S65775
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-1539 <KLI>
A;Cross-references: EMBL:X89761
R;Werr, W.
submitted to the EMBL Data Library, July 1995
A;Reference number: S72455
A;Accession: S72455
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-379, S', 381-1539 <WER>
A;Cross-references: EMBL:X89761; NID:g1143706; PIDN:CAA61910.1; PID:g1143707
C;Genetics:
A;Gene: Hox2b
C;Superfamily: unassigned homeobox proteins; homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;802-858/Domain: homeobox homology <HOX1>
F;1040-1096/Domain: homeobox homology <HOX2>

Query Match 35.8%; Score 44; DB 2; Length 1539;
Best Local Similarity 54.5%; Pred. No. 2; Mismatches 3; Indels 0; Gaps 0;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGTASCHFGPL 11
: : |||:
Db 1039 GDASKCHFGPI 1049

RESULT 29
S39069
vascactive intestinal peptide receptor VIP2 precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-Oct-1994 #sequence_revision 10 Nov-1995 #text_change 08-Oct-1999
C;Accession: S39069
R;Lutz, E.M.; Sheward, W.J.; West, K.M.; Morrow, J.A.; Fink, G.; Harmar, A.J.
FEBS Lett. 334, 3-8, 1993
A;Title: The VIP(2) receptor: molecular characterisation of a cDNA encoding a novel rece
A;Reference number: S39069; MUID:94039806; PMID:8224221
A;Accession: S39069
A;Molecule type: mRNA
A;Residues: 1-437 <LUT>
A;Cross-references: EMBL:Z25885; NID:g414188; PIDN:CAAS1104.1; PID:g414189
C;Superfamily: glucagon receptor
C;Keywords: G protein-coupled receptor; intestine; transmembrane protein

Query Match 35.4%; Score 43.5; DB 2; Length 437;
Best Local Similarity 56.2%; Pred. No. 99;
Matches 9; Conservative 1; Mismatches 5; Indels 1; Gaps 1;

QY 2 GTASCHFGPLTWV-CK 16
: : |||: ||
Db :87 GTLRCHDQPGSWVGCK 202

RESULT 30
B98236
exsI protein protein (AJ225561) [imported] - Agrobacterium tumefaciens (strain C58, Cere
C;Species: Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002
C;Accession: B98236
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blarchard, M.; Quorollo, B.; Goldman,
A.; Liu, F.; Woilam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: B98236
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-119 <KUR>
A;Cross-references: GB:AE007870; PIDN:AAK89412.1; PID:g15159269; GSPDB:GN00170

C;Genetics:
A;Gene: AGR_L1677
A;Map position: linear chromosome

Query Match 35.0%; Score 43; DB 2; Length 119;
Best Local Similarity 60.0%; Pred. No. 36;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 8 FGPLTWVCKP 17
||| |||: ||
Db 23 FGPATFLCRP 32

RESULT 31
S29714
guanine-nucleotide-releasing protein mss4 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Nov-1999
C;Accession: S29714
R;Burton, J.; Roberts, D.; Montaldi, M.; Novick, P.; de Camilli, P.
Nature 361, 464-467, 1993
A;Title: A mammalian guanine-nucleotide-releasing protein enhances function of yeast
A;Reference number: S29714; MUID:93156814; PMID:8429887
A;Accession: S29714
A;Molecule type: mRNA
A;Residues: 1-123 <BUR>
A;Cross-references: EMBL:X70496; NID:g313871; PIDN:CAA49904.1; PID:g313872
C;Genetics:
A;Gene: mss4

Query Match 35.0%; Score 43; DB 2; Length 123;
Best Local Similarity 50.0%; Pred. No. 37;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 4 ASCHFGPLTWVC 15
||| |||: ||
Db 95 ADCEIGPIGWHC 106

RESULT 32
I52427
guanine-nucleotide-releasing protein Mss4 - human
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C;Accession: I52427
R;Yu, H.; Schreiber, S.L.
Biochemistry 34, 9103-9110, 1995
A;Title: Cloning, Zn2+ binding, and structural characterization of the guanine nucle
A;Reference number: I52427; MUID:95345082; PMID:7619808
A;Accession: I52427
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-123 <RES>
A;Cross-references: GB:S78873; NID:g1037135; PIDN:AAB34955.1; PID:g1037136
C;Genetics:
A;Gene: GDB:MSS4
A;Cross-references: GDB:683578

Query Match 35.0%; Score 43; DB 2; Length 123;
Best Local Similarity 50.0%; Pred. No. 37;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 4 ASCHFGPLTWVC 15
||| |||: ||
Db 95 ADCEIGPIGWHC 106

RESULT 33
A46711
probable thioredoxin peroxidase (EC 1.11.1.-) PAGA - human
N;Alternate names: enhancer protein; heme-binding 23K protein (HBP23); natural kille
C;Species: Homo sapiens (man)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 02-Jun-2000
```


A;Molecule type: mRNA
A;Residues: 1-199 <KAW>
A;Cross-references: DDBJ:D21252; NID:G666969; PIDN:BAA04796.1; PID:G666970
A;Experimental source: osteoblastic cell line MC3T3-E1
A;Note: authors suggest, on the basis of homology to MER5 family, that this protein play
C;Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 prod
C;Keywords: glycoprotein
F;15-157/Domain: alkyl hydroperoxidase c22 protein homology <C22>
F;189/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 34.1%; Score 42; DB 2; Length 199;
Best Local Similarity 40.9%; Pred. No. 80;
Matches 9; Conservative 2; Mismatches 9; Indels 2; Gaps 1;

QY 1 GGTASCHFGPLTWCKP--QGG 20
| : ||| | : |||
Db 75 GASVDSHFCHLAWINTPKKGG 96

RESULT 43
I52425
Probable thioredoxin peroxidase (EC 1.11.1.1-) HBP23 - rat
N;Alternate names: heme-binding 23K protein (HBP23); proliferation associated protein PA
C;Species: Rattus norvegicus (Norway rat)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 02-Jun-2000
C;Accession: I52425
R;Iwahara, S.
Biochemistry 34, 13398-13406, 1995
A;Title: Purification, characterization, and cloning of a heme-binding protein (23 kDa)
A;Reference number: I52425; MUID:96027454; PMID:7577926
A;Accession: I52425
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-199 <IWA>
A;Cross-references: GB:D30035; NID:G1060976; PIDN:BAA06275.1; PID:G1060977
C;Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 prod
C;Keywords: heme; oxidoreductase
F;15-157/Domain: alkyl hydroperoxidase c22 protein homology <C22>

Query Match 34.1%; Score 42; DB 2; Length 199;
Best Local Similarity 40.9%; Pred. No. 80;
Matches 9; Conservative 2; Mismatches 9; Indels 2; Gaps 1;

QY 1 GGTASCHFGPLTWCKP--QGG 20
| : ||| | : |||
Db 75 GASVDSHFCHLAWINTPKKGG 96

RESULT 44
B59405
prolactin receptor short form Slb precursor, breast cancer cells T-47D - human
C;Species: Homo sapiens (man)
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Mar-2002
C;Accession: B59405; B49400
R;Hu, Z.Z.; Meng, J.; Dufau, M.L., 2001
J. Biol. Chem. 276, 41086-41094, 2001
A;Title: Isolation and characterization of two novel forms of the human prolactin recept
A;Reference number: A59405; MUID:21538812; PMID:11518703
A;Accession: B59405
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-288 <HU1>
A;Cross-references: GB:AF214012; PIDN:AF214012.1
R;Hu, Z.Z.
submitted to GenBank, December, 1999
A;Reference number: A49400
A;Accession: B49400
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-288 <HU2>
A;Cross-references: GB:AF214012; PIDN:AF214012.1
C;Comment: This is one of the short forms (Slb and Slb) of the human prolactin receptor g
ta-casein gene promoter activation, with Slb more effective than Slb. However, their lig

C;Genetics:
A;Gene: GDB:PRLR
A;Cross-references: GDB:120315; OMIM:176761
A;Map position: 5p13.3-5p13.1
C;Superfamily: cytokine receptor homology
C;Keywords: glycoprotein; transmembrane protein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-288/Product: prolactin receptor, short form Slb #status predicted <MAT>
F;36-221/Domain: cytokine receptor homology <CRS>
F;59,104,233/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 34.1%; Score 42; DB 2; Length 288;
Best Local Similarity 77.8%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGTASCHFG 9
| : ||| | : |||
Db 81 GGPNSCHFG 89

RESULT 45
T41373
hypothetical protein SPCC4G3.03 - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T41373
R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Hilbert, H.; Duesterhoeft, A.
submitted to the EMBL Data Library, March 1998
A;Reference number: Z21918
A;Accession: T41373
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-347 <WOO>
A;Cross-references: EMBL:Z97052; PIDN:CAB09780.1; GSPDB:GN00068; SPDB:SPCC4G3.03
A;Experimental source: strain 972h-; cosmid c4G3
C;Genetics:
A;Gene: SPDB:SPCC4G3.03
A;Map position: 3

Query Match 34.1%; Score 42; DB 2; Length 347;
Best Local Similarity 45.0%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 5; Indels 6; Gaps 1;

QY 1 GGTASCHFGPLTWCKPQGG 20
| : ||| | : |||
Db 252 GSIRSCHFTP-----PNCG 265

RESULT 46
A59405
prolactin receptor short form Slb precursor, breast cancer cells T-47D - human
C;Species: Homo sapiens (man)
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 23-Sep-2002
C;Accession: A59405; A49400
R;Hu, Z.Z.; Meng, J.; Dufau, M.L.
J. Biol. Chem. 276, 41086-41094, 2001
A;Title: Isolation and characterization of two novel forms of the human prolactin rec
A;Reference number: A59405; MUID:21538812; PMID:11518703
A;Accession: A59405
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-376 <HU1>
A;Cross-references: GB:AF214012; PIDN:AF214012.1
R;Hu, Z.Z.
submitted to GenBank, December, 1999
A;Reference number: A49400
A;Accession: A49400
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-376 <HU2>
A;Cross-references: GB:AF214012; PIDN:AF214012.1
C;Comment: This is one of the short forms (Slb and Slb) of the human prolactin recept
eta-casein gene promoter activation, with Slb less effective than Slb. However, their

ted COS-1 and HEK293 cells is due to rapid intracellular turnover of the receptor. #expe
C:Genetics:
A:Gene: GDB:PRLR
A:Cross-references: GDB:120315; OMIM:176761
A:Map position: 5p13.3-5p13.1
C:Superfamily: cytokine receptor transmembrane protein
C:Keywords: glycoprotein; signal sequence predicted <SIG>
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-376/Product: prolactin receptor, short form Sla #status predicted <MAT>
F:36-221/Domain: cytokine receptor homology <CRS>
F:59,104,233/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 34.1%; Score 42; DB 2; Length 376;
Best Local Similarity 77.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGTASCHFG 9
||| |||||
Db 81 GGPNSCHFG 89

RESULT 47
A35641
5-aminomidazole ribonucleotide carboxylase-5-aminomidazole-4-N-succinocarboxamide ribo
C:Species: Gallus gallus (chicken)
C:Date: 28-Sep-1990 #sequence_revision 28-Sep-1990 #text_change 21-Jul-2000
C:Accession: A35641
R:Chen, Z.; Dixon, J.E.; Zalkin, H.
Proc. Natl. Acad. Sci. U.S.A. 87, 3097-3101, 1990
A:Title: Cloning of a chicken liver cDNA encoding 5-aminomidazole ribonucleotide carbox
ylase from a chicken liver mutant.
A:Reference number: A35641; MUID:90222176; PMID:1691501
A:Accession: A35641
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-426 <CHE>
A:Cross-references: GB:M31764; NID:g211193; PIDN:AAA48601.1; PID:g211194
C:Superfamily: phosphoribosylaminimidazole carboxylase catalytic chain homology
F:267-398/Domain: phosphoribosylaminimidazole carboxylase catalytic chain homology <PCO

Query Match 34.1%; Score 42; DB 2; Length 426;
Best Local Similarity 46.2%; Pred. No. 1.6e+02;
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 4 ASCHFGLTWVCK 16
||| |||||
Db 90 AHCEMPIEWVCR 102

RESULT 48
E87375
conserved hypothetical protein CCL17 (imported) Caulobacter crescentus
C:Species: Caulobacter crescentus
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C:Accession: E87375
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.G.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: E87375
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-554 <STO>
A:Cross-references: GB:AE005673; NID:gl3422309; PIDN:AAK23001.1; GSPDB:GN00148
C:Genetics:
A:Gene: CCL17

Query Match 34.1%; Score 42; DB 2; Length 554;
Best Local Similarity 35.0%; Pred. No. 2e+02;
Matches 7; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 GGTASCHFGLTWVCKPQGG 20
||| |||||
Db 478 GGITASRFAQLFWLSRONGG 497

RESULT 49
A40144
prolactin receptor long form precursor, hepatoma and breast cancer cells - human
C:Species: Homo sapiens (man)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 01-Dec-2000
C:Accession: A40144; A57018
R:Boutin, J.M.; Edery, M.; Shirata, M.; Jolicoeur, C.; Lesueur, L.; Ali, S.; Gould, D.
Mol. Endocrinol. 3, 1455-1461, 1989
A:Title: Identification of a cDNA encoding a long form of prolactin receptor in human
A:Reference number: A40144; MUID:90114212; PMID:2558309
A:Accession: A40144

A:Molecule type: mRNA
A:Residues: 1-622 <BOU>
A:Cross-references: GB:M31661; NID:gl90361; PIDN:AAA60174.1; PID:gl90362
R:Fuh, G.; Wells, J.A.
J. Biol. Chem. 270, 13133-13137, 1995
A:Title: Prolactin receptor antagonists that inhibit the growth of breast cancer cell
A:Reference number: A57018; MUID:95286597; PMID:7768908
A:Accession: A57018
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 25-228, 'AW' <RES>
A:Cross-references: GB:S78505; NID:g999114; PIDN:AAB34470.1; PID:g999115
C:Genetics:
A:Gene: GDB:PRLR
A:Cross-references: GDB:120315; OMIM:176761
A:Map position: 5p13.3-5p13.1
C:Superfamily: cytokine receptor homology
C:Keywords: glycoprotein; transmembrane protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-622/Product: prolactin receptor, long form #status predicted <MAT>
F:36-221/Domain: cytokine receptor homology <CRS>
F:59,104,233/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 34.1%; Score 42; DB 2; Length 622;
Best Local Similarity 77.8%; Pred. No. 2.2e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGTASCHFG 9
||| |||||
Db 81 GGPNSCHFG 89

RESULT 50
T00636
hypothetical protein F21856.2 - human
C:Species: Homo sapiens (man)
C:Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 05-Nov-1999
C:Accession: T00636
R:Lamerdin, J.E.; McCready, P.M.; Skowronski, E.; Adamson, A.W.; Burkhardt-Schultz, K.
rgescu, A.; Avila, J.; Liu, S.; Bruce, R.; Quan, G.; Montgomery, M.; Ow, D.; Nolan, J.
submitted to the EMBL Data Library, January 1998
A:Description: Sequence analysis of a 3.5 Mb contig in 19p13.3 between CDC34 and D195
A:Reference number: Z14195
A:Accession: T00636
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-679 <LAM>
A:Cross-references: EMBL:AC004030; NID:g2804590; PIDN:AAB97620.1; PID:g2804592
C:Genetics:
A:Map position: 19p13.3
A:Introns: 594/1; 637/3; 650/3
A:Note: F21856_2

Query Match 34.1%; Score 42; DB 2; Length 679;
Best Local Similarity 36.8%; Pred. No. 2.4e+02;
Matches 7; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

Qy 2 GTASCHFGPLTWVCKPQG 20
Db 98 GARDAHQGRPTNALRPEDG 116

Search completed: November 5, 2003, 19:07:19
Job time : 25 secs

GenCore version 5.1.6
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CM protein - protein search, using sw model

Run on: November 5, 2003, 19:00:18 / Search time 11 Seconds
(without alignments)
85,503 Million cell updates/sec

Title: US-09-863-600E-19
Perfect score: 123
Sequence: 1 GGTASCHFGPLTWCKPQGG 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	58	47.2	19	1 LANC_STRSQ	P38655 streptomyc
2	55	44.7	19	1 DURC_STRGP	P36503 streptomyc
3	54	43.9	19	1 DURB_STRGW	P36502 streptomyc
4	50	40.7	19	1 DURA_STRGV	P36504 streptomyc
5	50	40.7	78	1 CINA_STRGV	P29827 streptomyc
6	47.5	38.6	731	1 HUTU_CAEEL	Q9nae2 caenorhabdi
7	45.5	37.0	498	1 HELI_HSVI1	Q00092 ictaluriid h
8	45	36.6	126	1 YMM2_YEAST	Q03207 saccharomyc
9	45	36.6	215	1 ERD2_ENTHI	Q44017 entamoeba h
10	45	36.6	346	1 YAMY_BACAL	P32819 bacillus ac
11	44.5	36.2	337	1 C5L2_HUMAN	Q9p296 homo sapien
12	44	35.8	387	1 YB96_YEAST	P38332 saccharomyc
13	44	35.8	421	1 P2X5_HUMAN	Q93086 homo sapien
14	44	35.8	522	1 GA6S_HUMAN	P34059 homo sapien
15	44	35.8	628	1 ABFA_ASPNG	P42254 aspergillus
16	44	35.8	735	1 AD02_MACFA	Q28478 macaca fasc
17	43.5	35.4	437	1 VIPS_RAT	P35000 rattus norv
18	43	35.0	123	1 MSS4_HUMAN	P47224 rattus norv
19	43	35.0	123	1 MSS4_MOUSE	Q91x96 mus musculu
20	43	35.0	123	1 MSS4_RAT	Q08326 rattus norv
21	43	35.0	199	1 PDX1_HUMAN	Q06830 homo sapien
22	43	35.0	397	1 YW04_CAEEL	Q10907 caenorhabdi
23	43	35.0	507	1 CRNA_EMENI	P22152 emericella
24	43	35.0	676	1 HUTU_HUMAN	Q96n76 homo sapien
25	43	35.0	676	1 HUTU_MOUSE	Q8vc12 mus musculu
26	42.5	34.6	96	1 Y189_ARCFU	Q30049 archaeoglob
27	42.5	34.6	347	1 IF32_YEAST	P40217 saccharomyc
28	42.5	34.6	478	1 SEP4_HUMAN	O43236 homo sapien
29	42	34.1	199	1 PDX1_MOUSE	P35700 mus musculu
30	42	34.1	199	1 PDX1_RAT	Q63716 rattus norv
31	42	34.1	426	1 PUR6_CHICK	P38024 gallus gall
32	42	34.1	502	1 PIV2_ADECR	Q96680 canine aden
33	42	34.1	622	1 PRLR_HUMAN	P16471 homo sapien

34	41.5	33.7	155	1 Y115_METJA	Q57579 methanococc
35	41.5	33.7	342	1 YPIX_CLOPE	P18020 clostridium
36	41.5	33.7	892	1 HIC1_MOUSE	Q9rlv5 mus musculu
37	41.5	33.7	982	1 POL_HTLV2	P03363 human t-cel
38	41.5	33.7	1133	1 VGLM_HANTB	P28728 hantaan vir
39	41.5	33.7	1133	1 VGLM_SEOUE	P33455 seoul virus
40	41.5	33.7	1133	1 VGLM_SEOUR	P17880 seoul virus
41	41.5	33.7	1134	1 VGLM_SEOUR	P28729 seoul virus
42	41	33.3	229	1 UNG_CHLMU	Q9pjd2 chlamydia m
43	41	33.3	229	1 UNG_CHLTR	O84613 chlamydia t
44	41	33.3	239	1 RNC_NEIMA	Q9jvd3 neisseria m
45	41	33.3	239	1 RNC_NEIMB	Q9k0c8 neisseria m
46	41	33.3	248	1 NAD5_MYCGE	P47623 mycoplasma
47	41	33.3	296	1 CYCG_RHOSH	Q53143 rhodobacter
48	41	33.3	330	1 TLX1_HUMAN	P31314 homo sapien
49	41	33.3	471	1 ORYB_ORYSA	P25777 oryza sativ
50	41	33.3	814	1 AD15_HUMAN	Q13444 homo sapien
51	41	33.3	815	1 AD15_MOUSE	O88839 mus musculu
52	41	33.3	873	1 LDVR_MOUSE	P98156 mus musculu
53	41	33.3	873	1 LDVR_RAT	P98166 rattus norv
54	41	33.3	906	1 RDL4_ARATH	Q9xifo arabidopsis
55	40.5	32.9	300	1 ERF5_ARATH	O80341 arabidopsis
56	40.5	32.9	437	1 VIPS_MOUSE	P41588 mus musculu
57	40.5	32.9	566	1 HEMA_IADU3	P03442 influenza a
58	40.5	32.9	1142	1 VGLM_PHV	P27315 prospect hi
59	40	32.5	71	1 CBA_CARPI	P38578 carnobacter
60	40	32.5	212	1 SSPA_HAEIN	P45207 haemophilus
61	40	32.5	343	1 LUM_CHICK	P51890 gallus gall
62	40	32.5	343	1 LUM_COTJA	Q9de67 coturnix co
63	40	32.5	359	1 LPFD_SALTY	P43663 salmonella
64	40	32.5	425	1 PUR6_HUMAN	P22234 homo sapien
65	40	32.5	425	1 PUR6_MOUSE	Q9dcl9 mus musculu
66	40	32.5	425	1 PUR6_RAT	P51583 rattus norv
67	40	32.5	443	1 PHOF_PSEAE	P23621 pseudomonas
68	40	32.5	468	1 TM11_HUMAN	Q96f44 homo sapien
69	40	32.5	511	1 AROF_LYCES	P37215 lycopersico
70	40	32.5	511	1 AROG_SOLTU	P37822 solanum tub
71	40	32.5	525	1 AROF_ARATH	P29976 arabidopsis
72	40	32.5	529	1 C792_ARATH	Q9flc8 arabidopsis
73	40	32.5	549	1 FAST_HUMAN	Q14296 homo sapien
74	40	32.5	694	1 UL31_HCMVA	P16848 human cytom
75	40	32.5	790	1 AD30_HUMAN	Q9ukf2 homo sapien
76	40	32.5	963	1 TRES_THETH	O06458 thermus the
77	40	32.5	1531	1 MRPI_HUMAN	P33527 homo sapien
78	39.5	32.1	153	1 SODC_HORSE	P00443 equus cabal
79	39.5	32.1	258	1 VSP1_TRIST	Q91516 trimeresuru
80	39.5	32.1	379	1 ADHX_ARATH	Q96533 arabidopsis
81	39.5	32.1	500	1 DPS1_YEAST	P39006 saccharomyc
82	39.5	32.1	548	1 IDD_MOUSE	P98154 mus musculu
83	39.5	32.1	550	1 HEMA_IADHK	P43257 influenza a
84	39.5	32.1	550	1 HEMA_IADH3	P11134 influenza a
85	39.5	32.1	896	1 POL_HTL1A	P03362 human t-cel
86	39	31.7	126	1 RNS6_PIG	P81649 sus scrofa
87	39	31.7	143	1 DSS4_YEAST	P32601 saccharomyc
88	39	31.7	144	1 NOGG_RAT	Q62809 rattus norv
89	39	31.7	192	1 MOBA_NEIMA	Q9juas neisseria m
90	39	31.7	192	1 MOBA_NEIMB	P58747 neisseria m
91	39	31.7	195	1 VPRT_BLVJ	P10270 bovine leuk
92	39	31.7	232	1 NOGG_HUMAN	Q13253 homo sapien
93	39	31.7	232	1 NOGG_MOUSE	P97466 mus musculu
94	39	31.7	265	1 MUR1_BACSH	P52972 bacillus sp
95	39	31.7	282	1 FU34_YEAST	P32907 saccharomyc
96	39	31.7	308	1 Y964_SYNY3	P72855 synechocyst
97	39	31.7	345	1 CC14_CAEEL	P18834 caenorhabdi
98	39	31.7	350	1 ADH_SCHPO	P00332 echinosacch
99	39	31.7	359	1 IDI2_METJA	Q58272 methanococc
100	39	31.7	410	1 PHT4_PSEPU	Q05184 pseudomonas

ALIGNMENTS

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LANC_STRSQ
ID LANC_STRSQ STANDARD; PRT; 19 AA.
AC P38655;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Lantibiotic ancovenin.
OS Streptomyces sp. (strain A647P-2).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1931;
RN [1]
RP SEQUENCE.
RA Wakamiya T., Uski Y., Shiba T., Kido Y., Motoki Y.;
RT "The structure of ancovenin, a new peptide inhibitor of angiotensin I
RT converting enzyme.";
RL Tetrahedron Lett. 26:665-668(1985).
CC -!- FUNCTION: ACTS AS INHIBITOR OF ANGIOTENSIN I CONVERTING ENZYME.
CC -!- PTM: Maturation of lantibiotics involves the enzymic conversion of
CC Thr, and Ser into dehydrated AA and the formation of thioether
CC bonds with cysteine or the formation of dialkylamine bonds with
CC lysine. This is followed by membrane translocation and cleavage of
CC the modified precursor.
CC -!- SIMILARITY: STRUCTURAL SIMILARITY TO OTHER TYPE B LANTIBIOTICS.
DR PIR; A61284; EWSMAN.
KW Antibiotic; Bacteriocin; Lantibiotic; D-amino acid; Thioether bond.
FT CROSSLNK 1 18 Beta-methylanthionine (Cys-Thr).
FT CROSSLNK 4 14 Lanthionine (Ser-Cys).
FT CROSSLNK 5 11 Beta-methylanthionine (Cys-Thr).
FT CROSSLNK 6 19 Lysinoalanine (Ser-Lys).
SQ SEQUENCE 19 AA; 2033 MW; F434299E2736286A CRC64;

Query Match 47.2%; Score 58; DB 1; Length 19;
Best Local Similarity 81.8%; Pred. No. 0.01;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 SCHFGPLTWVC 15
DB 4 SCSFGPLTWSC 14

RESULT 2
DURC_STRGP
ID DURC_STRGP STANDARD; PRT; 19 AA.
AC P36503;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Lantibiotic duramycin C.
OS Streptomyces griseoliteus.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
CX NCBI_TaxID=29306;
RN [1]
RP SEQUENCE.
RC STRAIN=R2107;
RX MEDLINE=91107436; PubMed=2125590;
RA Fredenhagen A., Fendrich G., Marki F., Marki W., Gruner J.,
RA Raschdorf F., Peter H.H.;
RT "Duramycins B and C, two new lanthionine containing antibiotics as
RT inhibitors of phospholipase A2. Structural revision of duramycin and
RT cinnamycin.";
RL J. Antibiot. 43:1403-1412(1990).
RN [2]
RP STRUCTURE BY NMR.
RX MEDLINE=93387292; PubMed=8375380;
RA Zimmermann N., Freund S., Fredenhagen A., Jung G.;
RT "Solution structure of the lantibiotics duramycin B and C.";
RL (In) Schneider C.H., Eberles A.N. (eds.);
RL Peptides 1992, pp.519-520, Escom Science Publishers, Leiden (1993).
RN [3]
RP STRUCTURE BY NMR.
RX MEDLINE=93387292; PubMed=8375380;
RA Zimmermann N., Freund S., Fredenhagen A., Jung G.;
RT "Solution structure of the lantibiotics duramycin B and C.";
RL (In) Schneider C.H., Eberles A.N. (eds.);
RL Peptides 1992, pp.519-520, Escom Science Publishers, Leiden (1993).
RN [3]
RP STRUCTURE BY NMR.
RX MEDLINE=93387292; PubMed=8375380;
RA Zimmermann N., Freund S., Fredenhagen A., Jung G.;
RT "Solution structure of the lantibiotics duramycin B and C.";
RL (In) Schneider C.H., Eberles A.N. (eds.);
RL Peptides 1992, pp.519-520, Escom Science Publishers, Leiden (1993).
RN [3]
RP STRUCTURE BY NMR.
RX MEDLINE=93387292; PubMed=8375380;
RA Zimmermann N., Freund S., Fredenhagen A., Jung G.;

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RT "Solution structures of the lantibiotics duramycin B and C.";
RL Eur. J. Biochem. 216:419-428(1993).
CC -!- FUNCTION: ACTS AS INHIBITOR OF PHOSPHOLIPASE A2.
CC -!- PTM: Maturation of lantibiotics involves the enzymic conversion of
CC Thr, and Ser into dehydrated AA and the formation of thioether
CC bonds with cysteine or the formation of dialkylamine bonds with
CC lysine. This is followed by membrane translocation and cleavage of
CC the modified precursor.
CC -!- SIMILARITY: STRUCTURAL SIMILARITY TO OTHER TYPE B LANTIBIOTICS.
KW Antibiotic; Bacteriocin; Lantibiotic; D-amino acid; Thioether bond.
FT CROSSLNK 1 18 Beta-methylanthionine (Cys-Thr).
FT CROSSLNK 4 14 Lanthionine (Ser-Cys).
FT CROSSLNK 5 11 Beta-methylanthionine (Cys-Thr).
FT CROSSLNK 6 19 Lysinoalanine (Ser-Lys).
SQ SEQUENCE 19 AA; 2007 MW; E2404ECE3F95286A CRC64;

Query Match 44.7%; Score 55; DB 1; Length 19;
Best Local Similarity 72.7%; Pred. No. 0.029;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 SCHFGPLTWVC 15
DB 4 SCSYGPLTWSC 14

RESULT 3
DURB_STRGW
ID DURB_STRGW STANDARD; PRT; 19 AA.
AC P36502;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Lantibiotic duramycin B.
OS Streptovorticillium sp. (strain R2075).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=35759;
RN [1]
RP SEQUENCE.
RX MEDLINE=91107436; PubMed=2125590;
RA Fredenhagen A., Fendrich G., Marki F., Marki W., Gruner J.,
RA Raschdorf F., Peter H.H.;
RT "Duramycins B and C, two new lanthionine containing antibiotics as
RT inhibitors of phospholipase A2. Structural revision of duramycin and
RT cinnamycin.";
RL J. Antibiot. 43:1403-1412(1990).
RN [2]
RP STRUCTURE BY NMR.
RA Zimmermann N., Freund S., Fredenhagen A., Jung G.;
RT "Solution structure of the lantibiotics duramycin B and C.";
RL (In) Schneider C.H., Eberles A.N. (eds.);
RL Peptides 1992, pp.519-520, Escom Science Publishers, Leiden (1993).
RN [3]
RP STRUCTURE BY NMR.
RX MEDLINE=93387292; PubMed=8375380;
RA Zimmermann N., Freund S., Fredenhagen A., Jung G.;
RT "Solution structures of the lantibiotics duramycin B and C.";
RL Eur. J. Biochem. 216:419-428(1993).
CC -!- FUNCTION: ACTS AS INHIBITOR OF PHOSPHOLIPASE A2.
CC -!- PTM: Maturation of lantibiotics involves the enzymic conversion of
CC Thr, and Ser into dehydrated AA and the formation of thioether
CC bonds with cysteine or the formation of dialkylamine bonds with
CC lysine. This is followed by membrane translocation and cleavage of
CC the modified precursor.
CC -!- SIMILARITY: STRUCTURAL SIMILARITY TO OTHER TYPE B LANTIBIOTICS.
KW Antibiotic; Bacteriocin; Lantibiotic; D-amino acid; Thioether bond.
FT CROSSLNK 1 18 Beta-methylanthionine (Cys-Thr).
FT CROSSLNK 4 14 Lanthionine (Ser-Cys).
FT CROSSLNK 5 11 Beta-methylanthionine (Cys-Thr).
FT CROSSLNK 6 19 Lysinoalanine (Ser-Lys).
SQ SEQUENCE 19 AA; 2063 MW; 0133445E27362F00 CRC64;

Query Match 43.9%; Score 54; DB 1; Length 19;

```


DE (Imidazole:propionate hydrolase).

GN Y51H4A.7.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;

OC Rhabditidae; Peloderinae; Caenorhabditis.

OX NCBI_TaxID=6239;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Bristol N2;

RA Sulston J.E.;

RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.

CC -!- CATALYTIC ACTIVITY: 3-(5-oxo-4,5-dihydro-3-H-imidazol-4-

CC y))propanoate = urocanate + H(2)O.

CC -!- COFACTOR: NAD (By similarity).

CC -!- PATHWAY: Histidine degradation; second step.

CC -!- SIMILARITY: BELONGS TO THE UROCANASE FAMILY.

CC -----

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CC -----

DR EMBL; AL132952; CAB61139.1; -.

DR WormPep; Y51H4A.7; CE22333.

DR InterPro; IPR000193; Urocanase.

DR Pfam; PF01175; Urocanase; 1.

DR ProDom; PD025423; Urocanase; 1.

DR PROSITE; PS01233; UROCANASE; 1.

KW Hypothetical protein; Histidine metabolism; Lyase; NAD.

SQ SEQUENCE 731 AA; 81523 MW; 891E1F61C9A604E6 CRC64;

Query Match 38.6%; Score 47.5; DB 1; Length 731;

Best Local Similarity 47.6%; Pred. No. 11;

Matches 10; Conservative 1; Mismatches 7; Indels 3; Gaps 1;

QY 1 GGTASCHFGPLTWVC---KPQ 18

Db 496 GGIIFSMGFGPRWVCTSGKPE 516

RESULT 7

HELI_HSVI1

ID HELI_HSVI1 STANDARD; PRT; 498 AA.

AC Q00092;

DT 01-DEC-1992 (Rel. 24, Created)

DT 01-DEC-1992 (Rel. 24, Last sequence update)

DT 01-DEC-1992 (Rel. 24, Last annotation update)

DE Probable helicase.

GN 25.

OS Ictalurid herpesvirus 1 (Channel catfish virus) (CCV).

OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;

OC Ictalurid Herpes-like viruses.

CX NCBI_TaxID=10401;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Auburn 1;

RX MEDLINE=92087490; PubMed=1727613;

RA Davison A.J.;

RL "Channel catfish virus: a new type of herpesvirus.";

RL Virology 186:9-14(1992).

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CC -----

DR EMBL; M75136; AAA88128.1; -.

DE PIR; H36788; HJBE11.

KW Helicase; ATP-binding.

FT NP_BIND 37 44 ATP (POTENTIAL).

SQ SEQUENCE 498 AA; 55761 MW; 445F61E9FE121AEF CRC64;

Query Match 37.0%; Score 45.5; DB 1; Length 498;

Best Local Similarity 56.2%; Pred. No. 16;

Matches 9; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

QY 1 GGTASCHFGPL-TWVC 15

Db 323 GGSASCRFGALIEVMC 338

RESULT 8

YMM2_YEAST

ID YMM2_YEAST STANDARD; PRT; 126 AA.

AC Q03207;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Hypothetical 14.5 kDa protein in PHO84-GTR1 intergenic region.

GN YML122C OR YM7056.04C.

OS Saccharomyces cerevisiae (Baker's yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.

OX NCBI_TaxID=4932;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=S288c / AB972;

RX PubMed=9169872;

RA Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T.,

RA Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S.,

RA Jagels K., Lye G., Moule S., Odell C., Pearson D., Rajandream M.A.,

RA Rice P., Skelton J., Walsh S., Whitehead S., Barrell B.G.;

RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome

RT XIII.";

RL Nature 387:90-93(1997).

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CC -----

DR EMBL; Z49218; CAA89158.1; -.

DR PIR; S54062; S54062.

DR SGD; S0004591; YML122C.

KW Hypothetical protein.

SQ SEQUENCE 126 AA; 14472 MW; EF8049302E3D235A CRC64;

Query Match 36.6%; Score 45; DB 1; Length 126;

Best Local Similarity 53.8%; Pred. No. 5.4;

Matches 7; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 TASCHFGPLTWVC 15

Db 53 TARCQFNSSSTWC 65

RESULT 9

ERD2_ENTHI

ID ERD2_ENTHI STANDARD; PRT; 215 AA.

AC O44017;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE ER lumen protein retaining receptor.

GN ERD2.

OS Entamoeba histolytica.

OC Eukaryota; Entamoebidae; Entamoeba.

```
OX NCBI_TaxID=5759;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HK-9;
RA Sanchez-Lopez R., Gama-Castro S., Ramos M.A., Merino E., Lizardi P.M.,
RA Alagon A.;
RT "Cloning and expression of the Entamoeba histolytica ERD2 gene.";
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Required for the retention of luminal endoplasmic
CC reticulum proteins. Determines the specificity of the luminal ER
CC protein retention system. Also required for normal vesicular
CC traffic through the Golgi (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO THE ERD2 FAMILY.
CC
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CC
CC EMBL; AJ002138; CAA05206.1;
DR InterPro; IPR000133; ERret_receptor.
DR Pfam; PF00660; ERLUMENR.
DR PRINTS; PR00660; ERLUMENR.
DR ProDom; PD005774; ERret_receptor; 1.
DR PROSITE; PS00951; ER_LUMEN_RECEPTOR_1; 1.
DR PROSITE; PS00952; ER_LUMEN_RECEPTOR_2; 1.
KW Endoplasmic reticulum; Transmembrane; Protein transport; Receptor.
FT DOMAIN 1 4 LUMENAL (POTENTIAL).
FT TRANSMEM 5 23 POTENTIAL.
FT DOMAIN 24 37 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 38 55 POTENTIAL.
FT DOMAIN 56 63 LUMENAL (POTENTIAL).
FT TRANSMEM 64 82 POTENTIAL.
FT DOMAIN 83 98 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 99 112 POTENTIAL.
FT DOMAIN 113 119 LUMENAL (POTENTIAL).
FT TRANSMEM 120 139 POTENTIAL.
FT DOMAIN 140 151 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 152 170 POTENTIAL.
FT DOMAIN 171 181 LUMENAL (POTENTIAL).
FT TRANSMEM 182 202 POTENTIAL.
FT DOMAIN 203 215 CYTOPLASMIC (POTENTIAL).
SQ SEQUENCE 215 AA; 25724 MW; 92CC39788711AB66 CRC64;
Query Match 36.6%; Score 45; DB 1; Length 215;
Best Local Similarity 46.2%; Pred. No. 8.7;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 3 TASCHFGPLTWVC 15
DB 174 TEQSYWSPLTWIC 186
RESULT 10
YAMY BACAD
ID YAMY BACAD STANDARD; PRT; 346 AA.
AC P32819;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 39.9 kDa protein in amylase 3' region.
OS Bacillus acidopulluliticus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=28030;
RN [1]
RP SEQUENCE FROM N.A.
RA Kelly A.P., Diderichsen B., Jorgensen S.T., McConnell D.J.;
RL Submitted (APR-1993) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: INVOLVED IN TRANSPORT (POTENTIAL).
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CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -!- SIMILARITY: STRONG, TO E.COLI YEIB, B.SUBTILIS YXAH (S14H) AND
CC B.SUBTILIS YRKO.
CC
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CC
CC EMBL; Z22520; CAA80248.1;
DR PIR; S34732; S34732.
DR Pfam; PF04171; DUF405; 1.
DR Pfam; PF04235; DUF418; 1.
KW Hypothetical protein; Transport; Transmembrane.
FT TRANSMEM 15 35 POTENTIAL.
FT TRANSMEM 55 75 POTENTIAL.
FT TRANSMEM 93 113 POTENTIAL.
FT TRANSMEM 139 159 POTENTIAL.
FT TRANSMEM 182 202 POTENTIAL.
FT TRANSMEM 229 249 POTENTIAL.
FT TRANSMEM 269 289 POTENTIAL.
FT TRANSMEM 295 315 POTENTIAL.
SQ SEQUENCE 346 AA; 39876 MW; A46DF6009FCF9B92 CRC64;
Query Match 36.6%; Score 45; DB 1; Length 346;
Best Local Similarity 77.8%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 6 CHFGPLTWV 14
DB 319 CKFGPLEWV 327
RESULT 11
C5L2_HUMAN
ID C5L2_HUMAN STANDARD; PRT; 337 AA.
AC Q9P236;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C5a anaphylatoxin chemotactic receptor C5L2.
GN GPR77 OR C5L2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Ohno M., Hirata T., Enomoto M., Araki T., Sato K., Ishimaru H.,
RA Takahashi T.A.;
RT "A putative chemoattractant receptor, C5L2 is expressed in granulocyte
RT and immature dendritic cells, but mature dendritic cells.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21105913; PubMed=11165367;
RA Lee D.K., George S.R., Cheng R., Nguyen T., Liu Y., Brown M.,
RA Lynch K.R., O'Dowd B.F.;
RT "Identification of four novel human G protein-coupled receptors
RT expressed in the brain.";
RL Brain Res. Mol. Brain Res. 86:13-22(2001).
RN [3]
RP FUNCTION.
RC TISSUE=Brain;
RX MEDLINE=21850712; PubMed=11773063;
RA Cain S.A., Monk P.N.;
RT "The orphan receptor C5L2 has high affinity binding sites for
RT complement fragments C5a and C5a des Arg(74).";
RL J. Biol. Chem. 277:7165-7169(2002).
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CC CC -!- FUNCTION: Receptor for the chemotactic and inflammatory peptide
CC CC anaphylatoxin C5a, C4a and C3a and their des arginated
CC CC derivatives. Couples weakly to Gi-mediated signaling pathways.
CC CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC CC -!- TISSUE SPECIFICITY: Frontal cortex, hippocampus, hypothalamus,
CC CC pons and liver.
CC CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC CC -----
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CC CC or send an email to license@isb-sib.ch).
CC CC -----
CC CC EMBL; AB038237; BAA95414.1; -
CC CC EMBL; AF317655; AAK12640.1; -
CC CC Genew; HGNC:4527; GPR77.
CC CC GO; GO:0016526; F:G-protein coupled receptor, unknown ligand . . . ; NAS.
CC CC InterPro; IPR000276; GPCR_Rhodpn.
CC CC Pfam; PF00001; 7tm1.1; 1.
CC CC PRINTS; PR00237; GPCRHOPOPSN.
CC CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
CC CC PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
CC CC KW G-protein coupled receptor; Transmembrane; Glycoprotein.
CC CC FT DOMAIN 1 38 EXTRACELLULAR (POTENTIAL).
CC CC TRANSMEM 39 61 1 (POTENTIAL).
CC CC DOMAIN 62 72 CYTOPLASMIC (POTENTIAL).
CC CC TRANSMEM 73 95 2 (POTENTIAL).
CC CC DOMAIN 96 114 EXTRACELLULAR (POTENTIAL).
CC CC TRANSMEM 115 137 3 (POTENTIAL).
CC CC DOMAIN 138 149 CYTOPLASMIC (POTENTIAL).
CC CC TRANSMEM 150 172 4 (POTENTIAL).
CC CC DOMAIN 173 202 EXTRACELLULAR (POTENTIAL).
CC CC TRANSMEM 203 225 5 (POTENTIAL).
CC CC DOMAIN 226 237 CYTOPLASMIC (POTENTIAL).
CC CC TRANSMEM 238 260 6 (POTENTIAL).
CC CC DOMAIN 261 274 EXTRACELLULAR (POTENTIAL).
CC CC TRANSMEM 275 294 7 (POTENTIAL).
CC CC DOMAIN 295 337 CYTOPLASMIC (POTENTIAL).
CC CC CARBOHYD 3 3 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CC DISULFID 107 186 BY SIMILARITY.
CC CC SEQUENCE 337 AA; 36080 MW; 53AF41B129FE8FE6 CRC64;
CC CC -----
CC CC Query Match 36.2%; Score 44.5; DB 1; Length 337;
CC CC Best Local Similarity 47.4%; Pred. No. 16;
CC CC Matches 9; Conservative 1; Mismatches 6; Indels 3; Gaps 1;
CC CC -----
CC CC QY 4 ASCHFGPLTWV---CKPQG 19
CC CC ||||| | | | | |
CC CC Db 217 ASCHSALLCWAARRCRPLG 235
CC CC -----
CC CC RESULT 12
CC CC YB96 YEAST
CC CC ID YB96 YEAST STANDARD; PRT; 387 AA.
CC CC AC P38332;
CC CC DT 01-OCT-1994 (Rel. 30, Created)
CC CC DT 01-OCT-1994 (Rel. 30, Last sequence update)
CC CC DT 01-OCT-1996 (Rel. 34, Last annotation update)
CC CC DE Hypothetical 43.3 kDa protein in ALG7-ENP; intergenic region.
CC CC GN YBR246W OR YBR1634.
CC CC OS Saccharomyces cerevisiae (Baker's yeast).
CC CC OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
CC CC OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
CC CC OX NCBI_TaxID=4932;
CC CC RN [1]
CC CC RP SEQUENCE FROM N.A.
CC CC RC STRAIN=S288c;
CC CC RA Aljinovic G., Pohl F.M., Pohl T.M.;
CC CC RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
CC CC -----

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CC CC -----
CC CC EMBL; Z36115; CAA85209.1; -
CC CC PIR; S46123; S46123.
CC CC SGD; S0000450; YBR246W.
CC CC InterPro; IPR001680; WD40.
CC CC Pfam; PF00400; WD40; 3.
CC CC KW Hypothetical protein.
CC CC SEQUENCE 387 AA; 43308 MW; 97CAFD285BC11456 CRC64;
CC CC -----
CC CC Query Match 35.8%; Score 44; DB 1; Length 387;
CC CC Best Local Similarity 69.2%; Pred. No. 21;
CC CC Matches 9; Conservative 0; Mismatches 2; Indels 2; Gaps 1;
CC CC -----
CC CC QY 4 ASCHFGPLTWVCK 16
CC CC ||||| | | | | |
CC CC Db 125 ASCHFSPLD--CK 135
CC CC -----
CC CC RESULT 13
CC CC P2X5_HUMAN
CC CC ID P2X5_HUMAN STANDARD; PRT; 421 AA.
CC CC AC Q93086; Q43450; Q75540; Q93087; Q9NZV0;
CC CC DT 01-NOV-1997 (Rel. 35, Created)
CC CC DT 16-OCT-2001 (Rel. 40, Last sequence update)
CC CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
CC CC DE P2X purinoceptor 5 (ATP receptor) (P2X5) (Purinergic receptor).
CC CC GN P2RX5 OR P2X5.
CC CC OS Homo sapiens (Human).
CC CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC CC OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CC CC OX NCBI_TaxID=9606;
CC CC RN [1]
CC CC RP SEQUENCE FROM N.A. (ISOFORMS A AND B).
CC CC RA Tokuyama Y., Mereu L., Chen X., Rouard M., Bell G.I.;
CC CC RT "Cloning of human P2X purinoceptor new subtype (P2X5).";
CC CC RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
CC CC RN [2]
CC CC RP SEQUENCE FROM N.A. (ISOFORM A).
CC CC RC TISSUE=Brain;
CC CC RX MEDLINE=98074936; PubMed=9414125;
CC CC RA Le K.-T., Paquet M., Nouel D., Babinski K., Seguela P.;
CC CC RT "Primary structure and expression of a naturally truncated human P2X
CC CC RL ATP receptor subunit from brain and immune system.";
CC CC FEBS Lett. 418:195-199(1997).
CC CC RN [3]
CC CC RP SEQUENCE FROM N.A. (ISOFORM B).
CC CC RC TISSUE=Brain;
CC CC RA Yu W., Gibbs R.A.;
CC CC RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
CC CC RN [4]
CC CC RP SEQUENCE FROM N.A. (ISOFORMS A AND B).
CC CC RX MEDLINE=20138496; PubMed=10673275;
CC CC RA Touchman J.W., Anikster Y., Dietrich N.L., Maduro V.V., McDowell G.,
CC CC RA Shetlersuk V., Bouffard G.G., Beckstrom-Sternberg S.M., Gahl W.A.,
CC CC RA Green E.D.;
CC CC RT "The genomic region encompassing the nephropathic cystinosis gene
CC CC RT (CTNS): complete sequencing of a 200-kb segment and discovery of a
CC CC RL novel gene within the common cystinosis-causing deletion.";
CC CC RL Genome Res. 10:165-173(2000).
CC CC CC -!- FUNCTION: RECEPTOR FOR ATP THAT ACTS AS A LIGAND GATED ION
CC CC CHANNEL.
CC CC CC -!- SUBUNIT: HOMO- OR HETEROPOLYMERS (BY SIMILARITY).
CC CC CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC CC CC -!- ALTERNATIVE PRODUCTS:
CC CC CC Event=Alternative splicing; Named isoforms=2;
CC CC Name=A;

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CC      isoid=Q93086-1; Sequence=Displayed;
CC      Name=B;
CC      isoid=Q93086-2; Sequence=VSP_004503;
CC      TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN BRAIN AND IMMUNE
CC      SYSTEM.
CC      -!- SIMILARITY: BELONGS TO THE P2X RECEPTOR FAMILY.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL; U49395; AAB08576.1; -
CC      EMBL; U49396; AAB08577.1; -
CC      EMBL; AF016709; AAC51931.1; -
CC      EMBL; AF070573; AAC28645.1; -
CC      EMBL; AF168787; AAF43106.1; ALT_SEQ.
CC      EMBL; AF168787; AAF43105.1; -
CC      Genew; HGNC:8536; P2RX5.
CC      MIM; 602836; -
CC      GO; GO:0005887; C:integral to plasma membrane; TAS.
CC      GO; GO:0005216; F:ion channel activity; TAS.
CC      GO; GO:0004889; F:transmembrane receptor activity; TAS.
CC      GO; GO:0007399; P:neurogenesis; TAS.
CC      GO; GO:0007165; P:signal transduction; TAS.
CC      GO; GO:0006832; P:small molecule transport; TAS.
CC      InterPro; IPR001429; P2X_receptor.
CC      Pfam; PF00864; P2X_receptor; 1.
CC      PRINTS; PR01307; P2XRECEPTOR.
CC      TIGRFAMS; TIGR00863; P2X; 1.
CC      PROSITE; PS01212; P2X_RECEPTOR; 1.
CC      Ionic channel; Transmembrane; Ion transport; Receptor; Glycoprotein;
KW      Alternative splicing.
FT      DOMAIN 1 30 CYTOPLASMIC (POTENTIAL).
FT      TRANSMEM 31 51 1 (POTENTIAL).
FT      DOMAIN 52 318 EXTRACELLULAR, CYSTEINE-RICH (POTENTIAL).
FT      TRANSMEM 319 339 2 (POTENTIAL).
FT      DOMAIN 340 421 CYTOPLASMIC (POTENTIAL).
FT      CARBOHYD 77 77 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD 202 202 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      VARSPLIC 97 120 Missing (in isoform B).
FT      CONFLICT 97 98 GE -> EK (IN REF. 1).
FT      CONFLICT 156 156 E -> G (IN REF. 2).
FT      CONFLICT 204 204 S -> SK (IN REF. 2).
FT      CONFLICT 236 237 VI -> IV (IN REF. 2).
FT      CONFLICT 250 250 E -> R (IN REF. 2).
FT      CONFLICT 329 329 F -> S (IN REF. 1).
FT      CONFLICT 351 351 E -> Q (IN REF. 1).
FT      CONFLICT 398 399 KR -> NV (IN REF. 1).
SQ      SEQUENCE 421 AA; 47103 MW; 6B47307AA14C2A6C CRC64;

Query Match 35.8%; Score 44; DB 1; Length 421;
Best Local Similarity 63.6%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      5 SCHFGPLTWVC 15
Db      218 SCHFGPKNHYC 228

RESULT 14
GA6S HUMAN
ID      GA6S HUMAN STANDARD; PRT; 522 AA.
AC      P34059;
DT      01-FEB-1994 (Rel. 28, Created)
DT      01-FEB-1994 (Rel. 28, Last sequence update)
DT      15-SEP-2003 (Rel. 42, Last annotation update)
DE      N-acetylgalactosamine-6-sulfatase precursor (EC 3.1.6.4) (N-
DE      acetylgalactosamine-6-sulfate sulfatase) (Galactose-6-sulfate
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DE      sulfatase) (GalNAc6S sulfatase) (Chondroitinsulfatase)
DE      (Chondroitinase).
GN      GALNS.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC      TISSUE=Placenta;
RX      MEDLINE=92095973; PubMed=1755850;
RA      Tomatsu S., Fukuda S., Masue M., Sukegawa K., Fukao T., Yamagishi A.,
RA      Hori T., Iwata H., Ogawa T., Nakashima Y., Hanyu Y., Hashimoto T.,
RA      Titani K., Oyama R., Suzuki M., Yagi K., Hayashi Y., Orii T.;
RT      "Morquio disease: isolation, characterization and expression of full-
RT      length cDNA for human N-acetylgalactosamine-6-sulfate sulfatase.";
RL      Biochem. Biophys. Res. Commun. 181:677-683(1991).
RN      [2]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=95095267; PubMed=8001980;
RA      Morris C.P., Guo X.H., Apostolou S., Hopwood J.J., Scott H.S.;
RT      "Morquio A syndrome: cloning, sequence, and structure of the human N-
RT      acetylgalactosamine 6-sulfatase (GALNS) gene.";
RL      Genomics 22:652-654(1994).
RN      [3]
RP      VARIANT MPS-IVA LYS-204.
RX      MEDLINE=92395122; PubMed=1522213;
RA      Fukuda S., Tomatsu S., Masue M., Sukegawa K., Iwata H., Ogawa T.,
RA      Nakashima Y., Hori T., Yamagishi A., Hanyu Y., Morooka K., Kiman T.,
RA      Hashimoto T., Orii T.;
RT      "Mucopolysaccharidosis type IVA. N-acetylgalactosamine-6-sulfate
RT      sulfatase exonic point mutations in classical Morquio and mild
RT      cases.";
RL      J. Clin. Invest. 90:1049-1053(1992).
RN      [4]
RP      VARIANTS MPS-IVA.
RX      MEDLINE=95397840; PubMed=7668283;
RA      Tomatsu S., Fukuda S., Cooper A., Wraith J.E., Maruf Rezvi G.,
RA      Yamagishi A., Yamada N., Kato Z., Isogai K., Sukegawa K., Kondo N.,
RA      Suzuki Y., Shimozaawa N., Orii T.;
RT      "Mucopolysaccharidosis IVA: identification of a common missense
RT      mutation I113F in the N-Acetylgalactosamine-6-sulfate sulfatase
RT      gene.";
RL      Am. J. Hum. Genet. 57:556-563(1995).
RN      [5]
RP      VARIANTS MPS-IVA.
RX      MEDLINE=95315929; PubMed=7795586;
RA      Ogawa T., Tomatsu S., Fukuda S., Yamagishi A., Maruf Rezvi G.,
RA      Sukegawa K., Kondo N., Suzuki Y., Shimozaawa N., Orii T.;
RT      "Mucopolysaccharidosis IVA: screening and identification of mutations
RT      of the N-acetylgalactosamine-6-sulfate sulfatase gene.";
RL      Hum. Mol. Genet. 4:341-349(1995).
RN      [6]
RP      VARIANTS MPS-IVA ARG-77; TRP-90; VAL-96; LEU-151; GLY-230 AND THR-291.
RX      MEDLINE=95359983; PubMed=7633425;
RA      Tomatsu S., Fukuda S., Cooper A., Wraith J.E., Maruf Rezvi G.,
RA      Yamagishi A., Yamada N., Kato Z., Isogai K., Sukegawa K., Kondo N.,
RA      Suzuki Y., Shimozaawa N., Orii T.;
RT      "Mucopolysaccharidosis type IVA: identification of six novel
RT      mutations among non-Japanese patients.";
RL      Hum. Mol. Genet. 4:741-743(1995).
RN      [7]
RP      VARIANT MPS-IVA SER-487.
RX      MEDLINE=96047158; PubMed=7581409;
RA      Tomatsu S., Fukuda S., Cooper A., Wraith J.E., Yamada N., Isogai K.,
RA      Kato Z., Sukegawa K., Kondo N., Suzuki Y., Shimozaawa N., Orii T.;
RT      "Two new mutations, Q473X and N487S, in a Caucasian patient with
RT      mucopolysaccharidosis IVA (Morquio disease).";
RL      Hum. Mutat. 6:195-196(1995).
RN      [8]
RP      VARIANTS MPS-IVA ALA-138; SER-151 AND LEU-151.
RX      MEDLINE=96216146; PubMed=8651279;
RA      Tomatsu S., Fukuda S., Yamagishi A., Cooper A., Wraith J.E., Hori T.,
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RA Kato Z., Yamada N., Isogai K., Sukegawa K., Kondo N., Suzuki Y.,
RA Shimoizawa N., Orii T.;
RT "Mucopolysaccharidosis IVA: four new exonic mutations in patients
RT with N-acetylgalactosamine-6-sulfate sulfatase deficiency.";
RL Am. J. Hum. Genet. 58:950-962(1996).
RN [9]
RN VARIANTS MPS-IVA CYS-94 AND VAL-97.
RX MEDLINE=96423834; PubMed=9826435;
RA Cole D.E.C., Fukuda S., Gordon B.A., Rip J.W., Lecouteur A.N.,
RA Rupar C.A., Tomatsu S., Ogawa T., Sukegawa K., Orii T.;
RT "Heteroallelic missense mutations of the galactosamine-6-sulfate
RT sulfatase (GALNS) gene in a mild form of Morquio disease (MPS IVA).";
RL Am. J. Med. Genet. 63:558-565(1996).
RN [10]
RN VARIANTS MPS-IVA.
RX MEDLINE=97442274; PubMed=9298823;
RA Bunge S., Kleijer W.J., Tylki-Szymanska A., Steglich C., Beck M.,
RA Tomatsu S., Fukuda S., Poorthuis B.J.H.M., Czartoryska B., Orii T.,
RA Gal A.;
RT "Identification of 31 novel mutations in the N-acetylgalactosamine-6-
RT sulfatase gene reveals excessive allelic heterogeneity among patients
RT with Morquio A syndrome.";
RL Hum. Mutat. 10:223-232(1997).
RN [11]
RN VARIANTS MPS-IVA.
RX MEDLINE=98041700; PubMed=9375852;
RA Tomatsu S., Fukuda S., Cooper A., Wraith J.E., Ferreira P.,
RA di Natale P., Tortora P., Fujimoto A., Kato Z., Yamada N., Isogai K.,
RA Yamagishi A., Sukegawa K., Suzuki Y., Shimoizawa N., Kondo N.,
RA Siy W.S., Orii T.;
RT "Fourteen novel mucopolysaccharidosis IVA producing mutations in
RT GALNS gene.";
RL Hum. Mutat. 10:368-375(1997).
RN [12]
RN VARIANTS MPS-IVA.
RX MEDLINE=98180718; PubMed=9521421;
RA Yamada N., Fukuda S., Tomatsu S., Muller V., Hopwood J.J., Nelson J.,
RA Kato Z., Yamagishi A., Sukegawa K., Kondo N., Orii T.;
RT "Molecular heterogeneity in mucopolysaccharidosis IVA in Australia
RT and Northern Ireland: nine novel mutations including T312S, a common
RT allele that confers a mild phenotype.";
RL Hum. Mutat. 11:202-208(1998).
RN [13]
RN VARIANTS SER-393 AND MET-488.
RX MEDLINE=98112415; PubMed=9452036;
RA Tomatsu S., Fukuda S., Cooper A., Wraith J.E., Yamagishi A., Kato Z.,
RA Yamada N., Isogai K., Sukegawa K., Suzuki Y., Shimoizawa N., Kondo N.,
RA Orii T.;
RT "Fifteen polymorphisms in the N-acetylgalactosamine-6-sulfate
RT sulfatase (GALNS) gene: diagnostic implications in Morquio disease.";
RL Hum. Mutat. Suppl. 1:S42-S46(1998).
CC -!- CATALYTIC ACTIVITY: Hydrolysis of the 6-sulfate groups of the N-
CC acetyl-D-galactosamine 6-sulfate units of chondroitin sulfate and
CC of the D-galactose 6-sulfate units of keratan sulfate.
CC -!- SUBUNIT: OLIGOMER OF DISULFIDE LINKED 40- AND 15-kDa POLYPEPTIDES.
CC -!- SUBCELLULAR LOCATION: Lysosomal.
CC -!- DISEASE: Defects in GALNS are the cause of mucopolysaccharidosis
CC type IVA (MPS-IVA) [MIM:253000]; also known as Morquio A syndrome.
CC MPS-IVA is characterized by specific spondyloepiphyseal dysplasia,
CC short trunk dwarfism, coxa valga, odontoid hypoplasia, corneal
CC opacities, preservation of intelligence, and excessive urinary
CC excretion of keratan sulfate and chondroitin-6-sulfate. Severely
CC affected patients usually die of cardiopulmonary disturbance or
CC cervical cord compression in the second or third decade of life.
CC -!- SIMILARITY: BELONGS TO THE SULFATASE FAMILY.
CC
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CC -----
DR EMBL; D17629; BAA04535.1; -
DR EMBL; D17616; BAA04535.1; JOINED.
DR EMBL; D17617; BAA04535.1; JOINED.
DR EMBL; D17618; BAA04535.1; JOINED.
DR EMBL; D17619; BAA04535.1; JOINED.
DR EMBL; D17620; BAA04535.1; JOINED.
DR EMBL; D17621; BAA04535.1; JOINED.
DR EMBL; D17622; BAA04535.1; JOINED.
DR EMBL; D17623; BAA04535.1; JOINED.
DR EMBL; D17624; BAA04535.1; JOINED.
DR EMBL; D17625; BAA04535.1; JOINED.
DR EMBL; D17626; BAA04535.1; JOINED.
DR EMBL; D17628; BAA04535.1; JOINED.
DR EMBL; U06088; AAC51350.1; -
DR EMBL; U06078; AAC51350.1; JOINED.
DR EMBL; U06079; AAC51350.1; JOINED.
DR EMBL; U06080; AAC51350.1; JOINED.
DR EMBL; U06081; AAC51350.1; JOINED.
DR EMBL; U06082; AAC51350.1; JOINED.
DR EMBL; U06083; AAC51350.1; JOINED.
DR EMBL; U06084; AAC51350.1; JOINED.
DR EMBL; U06085; AAC51350.1; JOINED.
DR EMBL; U06086; AAC51350.1; JOINED.
DR EMBL; U06087; AAC51350.1; JOINED.
DR PIR; JQ1299; KJHUG6.
DR HSSP; P15848; IFSU.
DR Genew; HGNC:4122; GALNS.
DR MIM; 253000; -
DR GO; GO:0003943; F:N-acetylgalactosamine-4-sulfatase activity; TAS.
DR InterPro; IPR000917; Sulfatase.
DR Pfam; PF00884; Sulfatase; 1.
DR PROSITE; PS00523; SULFATASE_1; 1.
DR PROSITE; PS00149; SULFATASE_2; 1.
KW Hydrolase; Glycoprotein; Signal; Lysosome; Mucopolysaccharidosis;
KW Disease mutation; Polymorphism; Dwarfism.
FT SIGNAL 1 26
FT CHAIN 27 522 N-ACETYL GALACTOSAMINE-6-SULFATASE.
FT MOD_RES 79 79 2-AMINO-3-OXOPROPIONIC ACID (BY
FT SIMILARITY).
FT CARBOHYD 204 204 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 423 423 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 47 47 G -> R (IN MPS-IVA; SEVERE FORM).
FT VARIANT 60 60 /FTID=VAR 007172
FT VARIANT 67 67 D -> N (IN MPS-IVA; MILD FORM).
FT VARIANT 67 67 /FTID=VAR 007173.
FT VARIANT 67 67 L -> M (IN MPS-IVA; ASSOCIATED WITH S-409
Query Match 35.8%; Score 44; DB 1; Length 522;
Best Local Similarity 43.8%; Pred. No. 28;
Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
QY 2 GTASCHFGPLTWCKP 17
Db 161 GSPNCHFGFYDNKARP 176
| : ||||| : |
RESULT 15
ABFA_ASPNG
ID ABFA_ASPNG STANDARD; PRT; 628 AA.
AC P42254;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Alpha-L-arabinofuranosidase A precursor (EC 3.2.1.55) (Arabinosidase
DE A) (ABF A).
GN ABFA.
OS Aspergillus niger.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5061;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 26-35 AND 63-77.

RC STRAIN=CBS 120.49 / N400;
RX MEDLINE=95093616; PubMed=8000538;
RA Flippin M.J.A., Visser J., van der Veen P., de Graaff L.H.;
RT "Arabinoxylanase gene expression in Aspergillus niger: indications for
RT coordinated regulation.";
RL Microbiology 140:2673-2682(1994).
CC -!- FUNCTION: ACTS ONLY ON SMALL LINEAR 1,5-ALPHA-LINKED
CC L-ARABINOFURANOSYL OLIGOSACCHARIDES.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of terminal non-reducing alpha-L-
CC arabinofuranoside residues in alpha-L-arabinosides.
CC -!- PATHWAY: Plant cell wall polysaccharide L-arabinan degradation.
CC -!- SIMILARITY: BELONGS TO FAMILY 51 OF GLYCOSYL HYDROLASES.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L29005; AAC41644.1; -;
DR EMBL; A27979; CAA01904.1; -;
KW Hydrolase; Glycosidase; Glycoprotein; Signal.
FT SIGNAL 1 25
FT CHAIN 26 628 ALPHA-L-ARABINOFURANOSIDASE A.
FT CARBOHYD 36 36 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 51 51 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 74 74 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 152 152 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 171 171 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 260 260 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 359 359 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 440 440 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 493 493 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 610 610 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 628 AA; 67832 MW; 4F3E476FF93468AD CRC64;

Query Match 35.8%; Score 44; DB 1; Length 628;
Best Local Similarity 47.1%; Pred. No. 33;
Matches 8; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 3 TASCHFGPLTWCKPQG 19
DB 535 TSUSDFGPLYWVASSAG 551

RESULT 16
AD02 MACFA STANDARD; PRT; 735 AA.
ID AD02 MACFA
AC Q28478; Q28472;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE ADAM2 precursor (A disintegrin and metalloproteinase domain 2)
GN (Fertilin beta subunit) (PH-30) (PH30) (PH30-beta).
OS ADAM2 OR FTNB.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=95260313; PubMed=7741716;
RA Perry A.C.F., Gichuhi P.M., Jones R., Hall L.;
RT "Cloning and analysis of monkey fertilin reveals novel alpha subunit
RT isoforms.";
RL Biochem. J. 307:843-850(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96341733; PubMed=8720115;

RA Ramarao C.S., Myles D.G., White J.M., Primakoff P.;
RT "Initial evaluation of fertilin as an immunoproteasome antigen and
RT molecular cloning of the cynomolgus monkey fertilin beta subunit.";
RL Mol. Reprod. Dev. 43:70-75(1996).
CC -!- FUNCTION: Sperm surface membrane protein that may be involved in
CC sperm-egg plasma membrane adhesion and fusion during
CC fertilization. Could have a direct role in sperm-zona binding or
CC migration of sperm from the uterus into the oviduct. Interactions
CC with egg membrane could be mediated via binding between its
CC disintegrin-like domain to one or more integrins receptors on the
CC egg. This is a non catalytic metalloprotease-like protein (By
CC similarity).
CC -!- SUBUNIT: Heterodimer with ADAM1/fertilin alpha.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed specifically in testis.
CC -!- DOMAIN: A tripeptide motif (FDE) within disintegrin-like domain
CC could be involved in the binding to egg integrin receptor and thus
CC could mediate sperm/egg binding (By similarity).
CC -!- PTM: The signal and the metalloprotease domain are cleaved during
CC the epididymal maturation of the spermatozoa (By similarity).
CC -!- SIMILARITY: Belongs to peptidase family M12B.
CC -!- SIMILARITY: Contains 1 EGF-like domain.
CC -!- SIMILARITY: Contains 1 disintegrin domain.
CC -----
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CC -----
DR EMBL; X77653; CAA54733.1; -;
DR EMBL; U33959; AAB52699.1; -;
DR PIR; G02937; G02937.
DR HSP; P17494; 1KST.
DR MEROPS; M12.950; -;
DR InterPro; IPR006586; ADAM_cysteine.
DR InterPro; IPR001762; Disintegrin.
DR InterPro; IPR002870; Pep_M12B_propep.
DR InterPro; IPR001590; Reprolysin.
DR Pfam; PF00200; disintegrin; 1.
DR Pfam; PF01562; Pep_M12B_propep; 1.
DR Pfam; PF01421; Reprolysin; 1.
DR ProDom; PD000664; Disintegrin; 1.
DR SMART; SM00608; ACR; 1.
DR SMART; SM00050; DISIN; 1.
DR PROSITE; PS00215; ADAM_MEPRO; 1.
DR PROSITE; PS00427; DISINTEGRIN_1; 1.
DR PROSITE; PS00214; DISINTEGRIN_2; 1.
DR PROSITE; PS00022; EGF_1; FALSE_NEG.
DR PROSITE; PS01186; EGF_2; FALSE_NEG.
KW Cell adhesion; Signal; Transmembrane; EGF-like domain; Glycoprotein.
FT SIGNAL 1 16 POTENTIAL.
FT PROPEP 17 174 BY SIMILARITY.
FT CHAIN 175 735 ADAM 2.
FT DOMAIN 17 686 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 687 707 POTENTIAL.
FT DOMAIN 708 735 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 175 382 METALLOPROTEASE-LIKE.
FT DOMAIN 383 475 DISINTEGRIN-LIKE.
FT DOMAIN 476 606 CYS-RICH.
FT DOMAIN 612 645 EGF-LIKE.
FT DISULFID 287 370 BY SIMILARITY.
FT DISULFID 329 354 BY SIMILARITY.
FT DISULFID 445 458 POTENTIAL.
FT DISULFID 616 627 BY SIMILARITY.
FT DISULFID 621 633 BY SIMILARITY.
FT DISULFID 635 644 BY SIMILARITY.
FT CARBOHYD 76 76 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 122 122 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 220 220 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 353 353 N-LINKED (GLCNAC. .) (POTENTIAL).

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FT CARBOHYD 459 459 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 566 566 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 723 723 S -> T (IN REF. 2).
SQ SEQUENCE 735 AA; 82357 MW; BE84BE115E1DCB53 CRC64;

Query Match 35.8%; Score 44; DB 1; Length 735;
Best Local Similarity 44.0%; Pred. No. 38;
Matches 11; Conservative 1; Mismatches 3; Indels 10; Gaps 2;

QY 1 GGTASC--HF-----GPLTWVC 15
D6 460 GTSACPENHFQTHGPGPNQWVC 484

RESULT 17
VIPS_RAT
ID VIPS_RAT STANDARD; PRT; 437 AA.
AC P15020;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Vasoactive intestinal polypeptide receptor 2 precursor (VIP-R-2)
DE (Pituitary adenylate cyclase activating polypeptide type III receptor)
DE (PACAP type III receptor) (PACAP-R-3).
GN VIPR2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
CX NCBI_TaxID=1016;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Olfactory bulb;
RX MEDLINE=94039806; PubMed=8224221;
RA Lutz E.-M., Sheward W.J., West K.M., Morrow J.A., Fink G.,
RA Hartmar A.J.;
RT "The VIP2 receptor: molecular characterisation of a cDNA encoding a
RT novel receptor for vasoactive intestinal peptide.";
RJ FEBS Lett. 334:3-8(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain cortex;
RX MEDLINE=95080140; PubMed=7988457;
RA Usdin T.B., Bonner T.I., Mezey E.;
RT "Two receptors for vasoactive intestinal polypeptide with similar
RT specificity and complementary distributions.";
RL Endocrinology 135:2662-2680(1994).
CC -1- FUNCTION: THIS IS A RECEPTOR FOR VIP AS WELL AS PACAP-38 AND -27,
CC THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH
CC ACTIVATE ADENYLATE CYCLASE. CAN BE COUPLED TO PHOSPHOLIPASE C.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF G PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
DR EMBL; Z25885; CAAB1104.1; -
DR EMBL; U09631; AAB60459.1; -
DR PIR; S39069; S39069.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR001879; hormn_receptor.
DR Pfam; PF00C02; 7tm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00008; Hormr; 1.
DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR PROSITE; PS02227; G_PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS02261; G_PROTEIN_RECEP_F2_4; 1.
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KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 437 VASOACTIVE INTESTINAL POLYPEPTIDE
FT RECEPTOR 2.
FT DOMAIN 23 125 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 126 150 1 (POTENTIAL).
FT DOMAIN 151 157 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 158 177 2 (POTENTIAL).
FT DOMAIN 178 202 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 203 226 3 (POTENTIAL).
FT TRANSMEM 227 239 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 240 261 4 (POTENTIAL).
FT TRANSMEM 262 278 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 279 302 5 (POTENTIAL).
FT TRANSMEM 303 327 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 328 347 6 (POTENTIAL).
FT TRANSMEM 348 359 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 360 379 7 (POTENTIAL).
FT DISULFID 201 270 BY SIMILARITY.
FT CARBOHYD 57 57 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 91 91 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 383 383 C -> R (IN REF. 2).
SQ SEQUENCE 437 AA; 49552 MW; 7E10218A9EE31360 CRC64;

Query Match 35.4%; Score 43.5; DB 1; Length 437;
Best Local Similarity 56.2%; Pred. No. 28;
Matches 9; Conservative 1; Mismatches 5; Indels 1; Gaps 1;

QY 2 GTASCHFGPLTWV-CK 16
D6 187 GTLRCHDQPGSWVGCK 202

RESULT 18
MSS4_HUMAN
ID MSS4_HUMAN STANDARD; PRT; 123 AA.
AC P47224; Q92992;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Guanine nucleotide exchange factor MSS4 (Rab interacting factor).
GN RABIF OR RASGRF3 OR MSS4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=95345082; PubMed=7619808;
RA Yu H., Schreiber S.L.;
RT "Cloning, Zn2+ binding, and structural characterization of the
RT guanine nucleotide exchange factor human Mss4.";
RL Biochemistry 34:9103-9110(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98110574; PubMed=9441742;
RA Mueller-Pillasch F., Zimmerhackl F., Lacher U., Schultz N.,
RA Hameister H., Varga G., Friess H., Buechler M., Adler G., Gress T.M.;
RT "Cloning of novel transcripts of the human guanine-nucleotide-exchange
RT factor Mss4: in situ chromosomal mapping and expression in pancreatic
RT cancer.";
RL Genomics 46:389-396(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
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FT METAL 26 26 ZINC (BY SIMILARITY).
FT METAL 94 94 ZINC (BY SIMILARITY).
FT METAL 97 97 ZINC (BY SIMILARITY).
SQ SEQUENCE 123 AA; 13915 MW; 73F3AECCDBE8B02 CRC64;

Query Match 35.0%; Score 43; DB 1; Length 123;
Best Local Similarity 50.0%; Pred. No. 11;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 4 ASCHFGPLTWVC 15
Db 95 ADCEIGPIGWHC 106

RESULT 20
MSS4 RAT STANDARD; PRT; 123 AA.
AC Q08326;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Guanine nucleotide exchange factor MSS4 (RAB interacting factor!).
GN RABIF OR MSS4.
CS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RX MEDLINE=93156814; PubMed=8429887;
RA Burton J., Roberts D., Montaldi M., Novick P., de Camilli P.;
RT "A mammalian guanine-nucleotide-releasing protein enhances function
of yeast secretory protein Sec4.";
RL Nature 361:464-467 (1993).
CC -!- FUNCTION: GUANINE-NUCLEOTIDE-RELEASING PROTEIN THAT ACTS ON
CC MEMBERS OF THE SCE4/YPT1/RAB SUBFAMILY. STIMULATES GDP RELEASE
CC FROM BOTH YPT1 AND RAB3A, BUT IS LESS ACTIVE ON THESE PROTEINS
CC THAN ON THE SEC4 PROTEIN. MIGHT PLAY A GENERAL ROLE IN VESICULAR
CC TRANSPORT.
CC -!- TISSUE SPECIFICITY: Ubiquitous.
CC -!- SIMILARITY: BELONGS TO THE DSS4/MSS4 FAMILY.
CC -----
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CC -----
DR EMBL; X70496; CAA49904.1; -
DR PIR; S29714; S29714.
DR PDB; 1HXR; 04-APR-01.
DR Pfam; PF04421; MSS4; 1.
KW Guanine-nucleotide releasing factor; Protein transport; Zinc;
KW 3D-structure.
FT METAL 23 23 ZINC (BY SIMILARITY).
FT METAL 26 26 ZINC (BY SIMILARITY).
FT METAL 94 94 ZINC (BY SIMILARITY).
FT METAL 97 97 ZINC (BY SIMILARITY).
FT STRAND 11 11
FT TURN 13 14
FT STRAND 16 17
FT STRAND 21 23
FT TURN 24 26
FT STRAND 29 31
FT TURN 33 34
FT STRAND 37 39
FT STRAND 43 46
FT STRAND 49 50
FT HELIX 51 54
FT TURN 56 57
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FT STRAND 62 65
FT STRAND 68 71
FT HELIX 74 76
FT STRAND 81 82
FT STRAND 86 86
FT TURN 87 88
FT STRAND 89 93
FT TURN 95 97
FT STRAND 99 100
FT STRAND 103 106
FT TURN 107 108
FT TURN 110 111
FT STRAND 113 116
FT HELIX 117 119
FT STRAND 120 123
SQ SEQUENCE 123 AA; 13928 MW; ACB7D07E2735811C CRC64;

Query Match 35.0%; Score 43; DB 1; Length 123;
Best Local Similarity 50.0%; Pred. No. 11;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 4 ASCHFGPLTWVC 15
Db 95 ADCEIGPIGWHC 106

RESULT 21
PDX1_HUMAN STANDARD; PRT; 199 AA.
AC Q06830; P35703;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Peroxiredoxin 1 (EC 1.11.1.1-) (Thioredoxin peroxidase 2) (Thioredoxin-
DE dependent peroxide reductase 2) (proliferation-associated protein PAG)
DE (Natural killer cell enhancing factor A) (NKEF-A).
GN PRDX1 OR TDPX2 OR PAGB OR PAGA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93265552; PubMed=8496166;
RA Prosperi M.T., Ferbus D., Karczynski I., Goubin G.;
RT "A human cDNA corresponding to a gene overexpressed during cell
RT proliferation encodes a product sharing homology with amoebic and
RT bacterial proteins.";
RL J. Biol. Chem. 268:11050-11056 (1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94299283; PubMed=8026862;
RA Shau H., Butterfield L.H., Chiu R., Kim A.;
RT "Cloning and sequence analysis of candidate human natural killer-
RT enhancing factor genes.";
RL Immunogenetics 40:129-134 (1994).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Urinary bladder;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
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RA Blakesley R.W., Touchman J.W., Green E.O., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [4]
 RP OXIDATION OF CYS-52.
 RX MEDLINE=22201787; PubMed=12059788;
 RA Wagner E., Luche S., Penna L., Chevallet M., van Dorsselaer A.,
 RA Leize-Wagner E., Rabilloud T.;
 RT "A method for detection of overoxidation of cysteines: peroxiredoxins
 are oxidized in vivo at the active-site cysteine during oxidative
 stress.";
 RT Biochem. J. 366:777-785(2002).
 RN [5]
 RP OXIDATION OF CYS-52.
 RX MEDLINE=22254876; PubMed=12161445;
 RA Yang K.S., Kang S.W., Woo H.A., Hwang S.C., Chae H.Z., Kim K.,
 RA Rhee S.G.;
 RT "Inactivation of human peroxiredoxin I during catalysis as the result
 of the oxidation of the catalytic site cysteine to cysteine-sulfinic
 acid.";
 RL J. Biol. Chem. 277:38029-38036(2002).
 CC -!- FUNCTION: Involved in redox regulation of the cell. Reduces
 peroxides with reducing equivalents provided through the
 thioredoxin system but not from glutaredoxin. May play an
 important role in eliminating peroxides generated during
 metabolism. Might participate in the signaling cascades of growth
 factors and tumor necrosis factor-alpha by regulating the
 intracellular concentrations of H(2)O(2).
 CC -!- SUBUNIT: Homodimer; disulfide-linked, upon oxidation (By
 similarity). May form heterodimers with AOP2.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- INDUCTION: Constitutively expressed in most human cells; is
 induced to higher levels upon serum stimulation in untransformed
 and transformed cells.
 CC -!- MISCELLANEOUS: The active site is the redox-active Cys-52 oxidized
 to Cys-SOH. Cys-SOH rapidly reacts with Cys-173-SH of the other
 subunit to form an intermolecular disulfide with a concomitant
 homodimer formation. The enzyme may be subsequently regenerated by
 reduction of the disulfide by thioredoxin.
 CC -!- MISCELLANEOUS: Irreversibly inactivated by overoxidation of Cys-52
 (to Cys-SO(2)H and Cys-SO(3)H) upon oxidative stress.
 CC -!- SIMILARITY: BELONGS TO THE AHPc/TSA FAMILY.
 CC -!- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
 WWW="http://www.infobiogen.fr/services/chronocancer/Genes/PAGID266.html".
 CC -----
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 CC -----
 DR EMBL; X67951; CAA48137.1; -;
 DR EMBL; L19184; AAA50464.1; -;
 DR EMBL; BC007063; AAH07063.1; -;
 DR EMBL; BC021683; AAH21683.1; -;
 DR PIR; A46711; A46711.
 DR HSSP; P30041; 1PRX.
 DR SWISS-2DPAGE; Q06830; HUMAN.
 DR Genew; HGNC:9352; PRDX1.
 DR MIM; 176763; -;
 DR GO; GO:0008283; P:cell proliferation; TAS.
 DR GO; GO:0001501; P:skeletal development; TAS.
 DR InterPro; IPR000866; AHPc-TSA.
 DR Pfam; PF00578; AHPc-TSA; 1.
 KW Antioxidant; Peroxidase; Oxidoreductase; Redox-active center.
 FT ACT SITE 52 52 CYS(INE) SULFENIC ACID INTERMEDIATE.
 FT DISULFID 52 52 INTERCHAIN (WITH C-173) (IN

FT DISULFID 173 173 LINKED FORM).
 FT INTERCHAIN (WITH C-52) (IN
 FT LINKED FORM).
 FT L -> P (IN REF. 2).
 FT CONFLICT 147 147
 FT CONFLICT 149 150 VG -> CC (IN REF. 2).
 FT CONFLICT 189 189 Q -> P (IN REF. 2).
 FT CONFLICT 191 191 S -> T (IN REF. 2).
 SQ SEQUENCE 199 AA; 22110 MW; 8F68E56D75BF5304 CRC64;
 Query Match 35.0%; Score 43; DB 1; Length 199;
 Best Local Similarity 45.5%; Pred. No. 16;
 Matches 10; Conservative 1; Mismatches 9; Indels 2; Gaps 1;
 QY 1 GGTASCHFGPLTWCKP--QGG 20
 | : ||| ||| |
 Db 75 GASVDSHFCHLAWVNTPKKGG 96
 RESULT 22
 YWO4_CAEEL STANDARD; PRT; 397 AA.
 ID YWO4_CAEEL
 AC Q10907;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Hypothetical 45.0 kDa protein AH9.4 in chromosome X.
 GN AH9.4.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Stellyes L., Gattung S.;
 RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -----
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 CC -----
 DR EMBL; U41270; AAA82442.1; -;
 DR PIR; T30088; T30088.
 DR WormPep; AH9.4; CE03860.
 KW Hypothetical protein; Transmembrane.
 FT TRANSMEM 6 26 POTENTIAL.
 FT TRANSMEM 165 185 POTENTIAL.
 FT TRANSMEM 211 231 POTENTIAL.
 FT TRANSMEM 311 331 POTENTIAL.
 FT TRANSMEM 349 369 POTENTIAL.
 SQ SEQUENCE 397 AA; 44968 MW; 96B2A189338A355F CRC64;
 Query Match 35.0%; Score 43; DB 1; Length 397;
 Best Local Similarity 50.0%; Pred. No. 31;
 Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;
 QY 1 GGTASCHFGPLTWCKPQ 18
 | ||| ||| : |
 Db 74 GITAGCHVGELVLLSKAQ 91
 RESULT 23
 CRNA_EMENI STANDARD; PRT; 507 AA.
 ID CRNA_EMENI
 AC P22152;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)

DE Nitrate transporter (Nitrate permease).
GN CRNA.
OS *Emmericella nidulans* (Aspergillus nidulans).
CC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
CC Eurotiales; Trichocomaceae; Emmericella.
OX NCBI_TaxID=162425;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91095428; PubMed=1986367;
RA Unkies S.E., Hawker K.L., Grieve C., Campbell E.I., Montague P.,
RA Kinghorn J.R.;
RT "crna encodes a nitrate transporter in Aspergillus nidulans.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:204-208(1991).
RN [2]
RP ERRATUM.
RA Unkies S.E., Hawker K.L., Grieve C., Campbell E.I., Montague P.,
RA Kinghorn J.R.;
RL Proc. Natl. Acad. Sci. U.S.A. 88:4564-4564(1991).
CC -!- FUNCTION: PERMEASE FOR NITRATE UPTAKE.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- INDUCTION: SUBJECT TO NITRATE AND NITRITE INDUCTION, AND NITROGEN
CC METABOLITE REPRESSION. CRNA EXPRESSION IS MEDIATED BY THE PRODUCTS
CC OF NIRA, AREA, AND NIAD.
CC
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CC
DR EMBL; M61125; AAA62125.1; -;
DR EMBL; U34382; AAA76713.1; -;
DR InterPro; IPR007114; MFS.
DR InterPro; IPR004737; NO3 transporter.
DR InterPro; IPR005828; Sub_transporter.
DR Pfam; PF00083; sugar_tr; 1.
DR TIGRFAMs; TIGR00886; 2A0108; 1.
KW Nitrate assimilation; Transport; Transmembrane.
FT DOMAIN 1 34 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 35 55 POTENTIAL.
FT DOMAIN 56 71 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 72 92 POTENTIAL.
FT DOMAIN 93 100 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 101 121 POTENTIAL.
FT DOMAIN 122 130 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 131 151 POTENTIAL.
FT DOMAIN 152 161 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 162 182 POTENTIAL.
FT DOMAIN 183 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 219 POTENTIAL.
FT DOMAIN 220 306 CYTOPLASMIC (HYDROPHILIC) (POTENTIAL).
FT TRANSMEM 307 327 POTENTIAL.
FT DOMAIN 328 357 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 358 378 POTENTIAL.
FT DOMAIN 379 389 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 390 410 POTENTIAL.
FT DOMAIN 411 417 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 418 438 POTENTIAL.
FT DOMAIN 439 507 CYTOPLASMIC (POTENTIAL).
SQ SEQUENCE 507 AA; 54925 MW; 4A3D3FA643F16952 CRC64;

Query Match 35.0%; Score 43; DB 1; Length 507;
Best Local Similarity 47.4%; Pred. No. 38;
Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 2 GTASCHFGPLTWCKPQGG 20
| : ||| ||| |||
Db 354 GKWAAMFGFLNIVCRPAGG 372

RESULT 24

HUTU_HUMAN
ID HUTU_HUMAN STANDARD; PRT; 676 AA.
AC Q96N76;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Probable urocanate hydratase (EC 4.2.1.49) (Urocanase)
DE (Imidazolonepropionate hydrolase).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S.,
RA Fukuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Ota T., Wakamatsu A., Ishii S., Yamamoto J.,
RA Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,
RA Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
RA Wagatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A.,
RA Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K.,
RA Masuho Y., Nagai K., Isogai T.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: 3-(5-oxo-4,5-dihydro-3-H-imidazol-4-yl)propanoate = urocanate + H(2)O.
CC -!- COFACTOR: NAD (By similarity).
CC -!- PATHWAY: Histidine degradation; second step.
CC -!- SIMILARITY: BELONGS TO THE UROCANASE FAMILY.
CC
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CC
DR EMBL; AK055862; BAB71032.1; -;
DR GK; Q96N76; -;
DR MIM; 276880; -;
DR InterPro; IPR000193; Urocanase.
DR Pfam; PF01175; Urocanase; 1.
DR ProDom; PD025423; Urocanase; 1.
DR PROSITE; PS01233; UROCANASE; 1.
KW Hypothetical protein; Histidine metabolism; Lyase; NAD.
SQ SEQUENCE 676 AA; 74830 MW; C940D3D068648D17 CRC64;

Query Match 35.0%; Score 43; DB 1; Length 676;
Best Local Similarity 53.3%; Pred. No. 50;
Matches 8; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 GG7ASCHFGPLTWVC 15
| : ||| |||
Db 439 GDIFSQGFGRFVVC 453

RESULT 25
HUTU_MOUSE
ID HUTU_MOUSE STANDARD; PRT; 676 AA.
AC Q8VC12;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Probable urocanate hydratase (EC 4.2.1.49) (Urocanase)
DE (Imidazolonepropionate hydrolase).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

RC TISSUE=Liver;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- CATALYTIC ACTIVITY: 3-(5-oxo-4,5-dihydro-3-H-imidazol-4-
CC yl)propanoate = urocanate + H(2)O.
CC -!- COFACTOR: NAD (By similarity).
CC -!- PATHWAY: Histidine degradation; second step.
CC -!- SIMILARITY: BELONGS TO THE UROCANASE FAMILY.
CC
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CC
CC -----
DR EMBL; BC022133; AAH22133.1; --
DR InterPro; IPR000193; Urocanase.
DR Pfam; PF01175; Urocanase; 1.
DR ProDom; PD025423; Urocanase; 1.
DR TIGRFAMs; TIGR01228; hutU; 1.
DR PROSITE; PS01233; UROCANASE; 1.
KW Hypothetical protein; Histidine metabolism; Lyase; NAD.
SQ SEQUENCE 676 AA; 74590 MW; 6C8645F6B4EA5455 CRC64;

Query Match 35.0%; Score 43; DB 1; Length 676;
Best Local Similarity 53.3%; Pred. No. 50;
Matches 8; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 GGTSASCHFGPLTWVC 15
Db 439 GDIFSGGFFRWVC 453

RESULT 26
Y189_ARCFU
ID Y189_ARCFU STANDARD; PRT; 96 AA.
AC Q30049;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein AF0189.
GN AF0189.
OS Archaeoglobus fulgidus.
OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
OC Archaeoglobaceae; Archaeoglobus.
OX NCBI_TaxID=2234;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RX MEDLINE=98049343; PubMed=9389475;
RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,

RA Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
RA Cotton M.D., Spriggs T., Artach P., Kaine B.P., Sykes S.M.,
RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
RA Venter J.C.;
RT "The complete genome sequence of the hyperthermophilic, sulphate-
RT reducing archaeon Archaeoglobus fulgidus."
RL Nature 390:364-370(1997).
CC
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CC
CC -----
DR EMBL; AE001093; AAB91047.1; --
DR PIR; E69273; E69273.
DR TIGR; AF0189; --
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 13 35 POTENTIAL.
SQ SEQUENCE 96 AA; 11332 MW; 22F660AA59C47795 CRC64;

Query Match 34.6%; Score 42.5; DB 1; Length 96;
Best Local Similarity 70.0%; Pred. No. 10;
Matches 7; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 6 CHFGPLTWVC 15
Db 50 CHFRP-SWVC 58

RESULT 27
IF32_YEAST
ID IF32_YEAST STANDARD; PRT; 347 AA.
AC P40217;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Eukaryotic translation initiation factor 3 39 kDa subunit (eIF3 p39)
DE (Translation initiation factor eIF3, p39 subunit).
GN TIF34 OR YMR146C OR YM9375.16C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=W303D;
RX MEDLINE=97127370; PubMed=8972194;
RA Naranda T., Kainuma M., Macmillan S.E., Hershey J.W.B.;
RT "The 39-kilodalton subunit of eukaryotic translation initiation
RT factor 3 is essential for the complex's integrity and for cell
RT viability in Saccharomyces cerevisiae."
RL Mol. Cell. Biol. 17:145-153(1997).
RN [2]_
RP SEQUENCE FROM N.A.
RC STRAIN=S288c / AB972;
RX PubMed=9169872;
RA Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T.,
RA Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S.,
RA Jagels K., Lye G., Moule S., Odell C., Pearson D., Rajandream M.A.,
RA Rice P., Skelton J., Walsh S., Whitehead S., Barrell B.G.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome
RT XIII."
RL Nature 387:90-93(1997).
CC -!- FUNCTION: EIF-3 DISSOCIATES RIBOSOMES, PROMOTES INITIATOR MET-TRNA
CC AND MRNA BINDING.

```
CC -!- SUBUNIT: EIF-3 IS COMPOSED OF UP TO 8 DIFFERENT SUBUNITS.
CC -!- SIMILARITY: Contains 5 WD repeats.
CC -----
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CC -----
CC EMBL; U56937; AAC49616.1; -.
DR EMBL; Z47071; CAA87361.1; -.
DR PIR; S50403; S50403.
DR SGD; S0004754; TIF34.
DR GO; GO:0005852; C:eukaryotic translation initiation factor 3 . . . ; IDA.
DR GO; GO:0003743; F:translation initiation factor activity; IDA.
DR GO; GO:0006413; P:translational initiation; IDA.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 5.
DR ProDom; PDC00018; WD40; 1.
DR SMART; SM00320; WD40; 5.
DR PROSITE; PS00678; WD_REPEATS_1; 1.
DR PROSITE; PS50082; WD_REPEATS_2; 3.
DR PROSITE; PS50294; WD_REPEATS_REGION; 2.
KW Initiation factor; Protein biosynthesis; Repeat; WD repeat.
FT REPEAT 8 38 WD 1.
FT REPEAT 50 80 WD 2.
FT REPEAT 149 181 WD 3.
FT REPEAT 194 224 WD 4.
FT REPEAT 291 321 WD 5.
SQ SEQUENCE 347 AA; 38755 MW; E6C0D09275E87622 CRC64;

Query Match: 34.6%; Score 42.5; DB 1; Length 347;
Best Local Similarity 52.6%; Pred. No. 32;
Matches 10; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

QY 2 GTASCHFGPLTWVC-KPOG 19
Dy 28' GRVQGHFGPNTVAISPG 305

RESULT 28
SEP4 HUMAN
ID SEP4 HUMAN STANDARD; PRG; 478 AA.
AC C43236; Q9UM58;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Septin 4 (Peanut-like protein 2) (Brain protein H4; (cell division
DE control-related protein 2) (hCDCREL-2) (Bradykin beta) (CE5B3 beta)
DE (Cerebral protein-7) (hucep-7).
GN SEPT4 OR PNUTL2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zha D., Hu G.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99107819; PubMed=9889007;
RA Paavola P., Horelli-Kuitunen N., Paotie A., Peltonen J.;
RT "Characterization of a novel gene, PNUTL2, on human chromosome
RL Genomics 55:122-125(1999).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS A AND B).
RC TISSUE=Brain;
RA Zieger B., Ware J.;
PL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
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RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=21402352; PubMed=11511094;
RA Tanaka M., Tanaka T., Kijima H., Itoh J., Matsuda T., Hori S.,
RA Yamamoto M.;
RT "Characterization of tissue- and cell-type-specific expression of a
RT novel human septin family gene, Bradeion.";
RL Biochem. Biophys. Res. Commun. 286:547-553(2001).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM A).
RC TISSUE=Brain;
RA Yoshimoto M., Yazaki M., Matsumoto K., Takayama K.;
RT "Molecular cloning of a new GTP binding protein from human brain.";
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM B).
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: INVOLVED IN CYTOKINESIS (POTENTIAL).
CC -!- SUBUNIT: MAY ASSEMBLE INTO A MULTICOMPONENT STRUCTURE.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=A;
CC IsoId=O43236-1; Sequence=Displayed;
CC Name=B;
CC IsoId=O43236-2; Sequence=VSP 006050;
CC -!- SIMILARITY: BELONGS TO THE SEPTIN FAMILY.
CC -----
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CC -----
CC EMBL; AF035811; AAB88512.1; -.
DR EMBL; AF073312; AAC25673.1; -.
DR EMBL; U88829; AAD00653.1; -.
DR EMBL; U88870; AAD00657.1; -.
DR EMBL; AB008753; BAB70695.1; -.
DR EMBL; D89278; BAB46922.1; -.
DR EMBL; BC018056; AAH18056.1; -.
DR Genew; HGNC:9165; PNUTL2.
DR MIM; 603696; -.
DR GO; GO:0003924; F:GTPase activity; TAS.
DR GO; GO:0005198; F:structural molecule activity; TAS.
DR GO; GO:0016288; P:cytokinesis; TAS.
DR InterPro; IPR000038; GTP_Cell_Div.
DR Pfam; PF00735; GTP_CDC; 1.
DR ProDom; PD002565; GTP_Cell_Div; 1.
KW Cell division; GTP-binding; Coiled coil; Alternative splicing.
```

```
FT NP_BIND 151 158 GTP (POTENTIAL).
FT DOMAIN 447 478 COILED COIL (POTENTIAL).
FT VARSPLIC 1 20 MDRSLGWQNSVPEDETEAG -> M (in isoform B).
FT /FTID=VSP 006050.
SQ SEQUENCE 478 AA; 55098 MW; 2F08D3611EF6523D CRC64;

Query Match 34.6%; Score 42.5; DB 1; Length 478;
Best Local Similarity 50.0%; Pred. No. 43;
Matches 10; Conservative 1; Mismatches 4; Indels 5; Gaps 2;

Qy 2 GTASCHFGP---LTWVCKPQ 18
Db 43 GNASCH--PPEAKTWASRPQ 60

RESULT 29
PDX1_MOUSE
ID PDX1_MOUSE STANDARD; PRT; 199 AA.
AC P35700;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Peroxiredoxin 1 (EC 1.11.1.-) (Thioredoxin peroxidase 2) (Thioredoxin-
DE dependent peroxide reductase 2) (Osteoblast specific factor 3) (OSF-3)
DE (Macrophage 23 kDa stress protein).
GN PRDX1 OR TDPX2 OR MSP23 OR PAGA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RC TISSUE=Peritoneal macrophage;
RX MEDLINE=93366771; PubMed=8360158;
RA Ishii T., Yamada M., Sato H., Matsue M., Taketani S., Nakayama K.,
RA Sugita Y., Bannai S.;
RT "Cloning and characterization of a 23-kDa stress-induced mouse
RT peritoneal macrophage protein."
RL J. Biol. Chem. 268:18633-18636(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Osteoblast;
RX MEDLINE=94375405; PubMed=8089076;
RA Kawai S., Takeshita S., Okazaki M., Kikuno R., Kudo A., Amann E.;
RT "Cloning and characterization of OSP-3, a new member of the MBR5
RT family, expressed in mouse osteoblastic cells."
RL J. Biochem. 115:641-643(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvJ; TISSUE=Liver;
RA Hino K., Sato H., Bannai S.;
RT "Characterization of mouse type I peroxiredoxin gene and
RT pseudogenes."
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Involved in redox regulation of the cell. Reduces
CC peroxides with reducing equivalents provided through the
CC thioredoxin system but not from glutaredoxin. May play an
CC important role in eliminating peroxides generated during
CC metabolism. Might participate in the signaling cascades of growth
CC factors and tumor necrosis factor-alpha by regulating the
CC intracellular concentrations of H(2)O(2).
CC -!- SUBUNIT: Homodimer; disulfide-linked, upon oxidation (By
CC similarity). May form heterodimers with AOP2.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- TISSUE SPECIFICITY: FOUND IN VARIOUS TISSUES; HIGH CONCENTRATION
CC IN LIVER.
CC -!- INDUCTION: BY OXIDATIVE AND SULFHYDRYL-REACTIVE AGENTS.
CC -!- MISCELLANEOUS: The active site is the redox-active Cys-52 oxidized
CC to Cys-SOH. Cys-SOH rapidly reacts with Cys-173-SH of the other
CC subunit to form an intermolecular disulfide with a concomitant
CC homodimer formation. The enzyme may be subsequently regenerated by
CC reduction of the disulfide by thioredoxin (By similarity).
CC -!- MISCELLANEOUS: Irreversibly inactivated by overoxidation of Cys-52
```

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CC (to Cys-SO3H) upon oxidative stress (By similarity).
CC -!- SIMILARITY: BELONGS TO THE AHPc/TSA FAMILY.
CC -----
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CC -----
CC EMBL; D16142; BAA03713.1; -
CC EMBL; D21252; BAA04796.1; -
CC EMBL; AB023564; BAA86992.1; -
CC EMBL; AB023560; BAA86992.1; JOINED.
CC EMBL; AB023561; BAA86992.1; JOINED.
CC EMBL; AB023562; BAA86992.1; JOINED.
CC EMBL; AB023563; BAA86992.1; JOINED.
CC PIR; A48513; A48513.
CC HSP; P30041; LPRX.
CC SWISS-2DPAGE; P35700; MOUSE.
CC MGD; MGI:99523; Prdx1.
CC GO; GO:0006979; P:response to oxidative stress; IDA.
CC InterPro; IPR000866; AhpC-TSA.
CC Pfam; PF00578; AhpC-TSA; 1.
KW Antioxidant; Peroxidase; Oxidoreductase; Redox-active center.
FT ACT_SITE 52 52 CYSTEINE SULFENIC ACID INTERMEDIATE
FT DISULFID 52 52 (BY SIMILARITY).
FT DISULFID 173 173 INTERCHAIN (WITH C-173) (IN
FT DISULFID 173 173 LINKED FORM) (BY SIMILARITY).
FT DISULFID 173 173 INTERCHAIN (WITH C-52) (IN
FT DISULFID 173 173 LINKED FORM) (BY SIMILARITY).
SQ SEQUENCE 199 AA; 22176 MW; BEF5C995A86124D1 CRC64;

Query Match 34.1%; Score 42; DB 1; Length 199;
Best Local Similarity 40.9%; Pred. No. 23;
Matches 9; Conservative 2; Mismatches 9; Indels 2; Gaps 1;

Qy 1 GGTASCHFGPLTWVCKP--QGG 20
Db 75 GASVDSHFCHLAWINTPKQGG 96

RESULT 30
PDX1_RAT
ID PDX1_RAT STANDARD; PRT; 199 AA.
AC Q63716;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Peroxiredoxin 1 (EC 1.11.1.-) (Thioredoxin peroxidase 2) (Thioredoxin-
DE dependent peroxide reductase 2) (Heme-binding 23 kDa protein) (HBP23).
GN PRDX1 OR TDPX2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Liver;
RX MEDLINE=96027454; PubMed=7577926;
RA Iwahara S.-I., Satoh H., Song D.-X., Webb J., Burlingame A.L.,
RA Nagae Y., Muller-Eberhard U.;
RT "Purification, characterization, and cloning of a heme-binding
RT protein (23 kDa) in rat liver cytosol."
RL Biochemistry 34:13398-13406(1995).
CC -!- FUNCTION: Involved in redox regulation of the cell. Reduces
CC peroxides with reducing equivalents provided through the
CC thioredoxin system but not from glutaredoxin. May play an
CC important role in eliminating peroxides generated during
CC metabolism. Might participate in the signaling cascades of growth
CC factors and tumor necrosis factor-alpha by regulating the
CC intracellular concentrations of H(2)O(2).
```

CC -!- SUBUNIT: Homodimer; disulfide-linked, upon oxidation (By
 CC similarity). May form heterodimers with AOP2.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- MISCELLANEOUS: The active site is the redox-active Cys-52 oxidized
 CC to Cys-SOH. Cys-SOH rapidly reacts with Cys-173-SH of the other
 CC subunit to form an intermolecular disulfide with a concomitant
 CC homodimer formation. The enzyme may be subsequently regenerated by
 CC reduction of the disulfide by thioredoxin (By similarity).
 CC -!- MISCELLANEOUS: Irreversibly inactivated by overoxidation of Cys-52
 CC (to Cys-SO₃H) upon oxidative stress (By similarity).
 CC -!- SIMILARITY: BELONGS TO THE AHPc/TSA FAMILY.
 CC
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 CC
 CC EMBL: D3C035; BAA06275.1; -
 CC PIR: I52425; I52425.
 CC PDB: 1QQ2; 29-OCT-99.
 CC InterPro: IPR000866; AhpC-TSA.
 CC Pfam: PF00578; AhpC-TSA; 1.
 CC Antioxidant; Peroxidase; Oxidoreductase; Redox-active center;
 KW 3D-structure.
 FT ACT_SITE 52 52 CYSTEINE SULFENIC ACID INTERMEDIATE
 FT (BY SIMILARITY).
 FT DISULFID 52 52 INTERCHAIN (WITH C-173) (IN
 FT LINKED FORM) (BY SIMILARITY).
 FT DISULFID 173 173 INTERCHAIN (WITH C-52) (IN
 FT LINKED FORM) (BY SIMILARITY).
 FT SEQUENCE 199 AA; 22109 MW; 3DF2D4ABA8A776DA CRC64;
 Query Match 34.1%; Score 42; DB 1; Length 199;
 Best Local Similarity 40.9%; Pred. No. 23;
 Matches 9; Conservative 2; Mismatches 9; Indels 2; Gaps 1;
 QY 1 GGTASCHFGPLTWCKP--QGG 20
 | : ||| | : |||
 Db 75 GASVDSHFCHLAWINTPKKQGG 96
 RESULT 31
 PUR6 CHICK
 ID PUR6 CHICK STANDARD; PRT; 426 AA.
 AC P38024; P87465;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Multifunctional protein ADE2 [includes: Phosphoribosylaminoimidazole-
 DE succinocarboxamide synthase (EC 6.3.2.6) (SAICAR synthetase);
 DE Phosphoribosylaminoimidazole carboxylase (EC 4.1.1.21) (AIR
 DE carboxylase) (AIRC)].
 GN AIRC.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 OC Gallus.
 CC NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=90222176; PubMed=1691501;
 RA Chen Z.D., Dixon J.E., Zalkin H.;
 RT "Cloning of a chicken liver cDNA encoding 5-aminoimidazole
 RT ribonucleotide carboxylase and 5-aminoimidazole-4-N-succinocarboxamide
 RT ribonucleotide synthetase by functional complementation of Escherichia
 RT coli pur mutants."
 RL Proc. Natl. Acad. Sci. U.S.A. 87:3097-3101(1990).
 RN [2]
 RP SEQUENCE OF 1-30 FROM N.A.

RX MEDLINE=93330273; PubMed=8336716;
 RA Gavalas A., Dixon J.E., Brayton K.A., Zalkin H.;
 RT "Coexpression of two closely linked avian genes for purine nucleotide
 RT synthesis from a bidirectional promoter."
 RL Mol. Cell. Biol. 13:4784-4792(1993).
 CC -!- CATALYTIC ACTIVITY: ATP + 5-amino-1-(5-phospho-D-
 CC ribosyl)imidazole-4-carboxylate + L-aspartate = ADP + phosphate +
 CC (S)-2-[5-amino-1-(5-phospho-D-ribosyl)imidazole-4-
 CC carboxamidolsuccinate].
 CC -!- CATALYTIC ACTIVITY: 5-amino-1-(5-phospho-D-ribosyl)imidazole-4-
 CC carboxylate = 5-amino-1-(5-phospho-D-ribosyl)imidazole + CO(2).
 CC -!- PATHWAY: De novo purine biosynthesis; sixth step.
 CC -!- PATHWAY: De novo purine biosynthesis; seventh step.
 CC -!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE SAICAR
 CC SYNTHETASE FAMILY.
 CC -!- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE AIR
 CC CARBOXYLASE FAMILY.
 CC
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 CC
 CC EMBL: M31764; AAA48601.1; -
 CC EMBL: L12533; AAA17894.1; -
 CC PIR: A35641; A35641.
 CC InterPro: IPR000031; AIR_carboxyl.
 CC InterPro: IPR001636; SAICAR_synt.
 CC Pfam: PF00731; AIRC; 1.
 CC Pfam: PF01259; SAICAR_synt; 1.
 CC ProDom: PD02193; AIR_carboxyl; 1.
 CC ProDom: PD003043; SAICAR_synt; 1.
 CC TIGRfam: TIGR01162; purE; 1.
 CC PROSITE: PS01057; SAICAR_SYNTHETASE_1; 1.
 CC PROSITE: PS01058; SAICAR_SYNTHETASE_2; 1.
 KW Multifunctional enzyme; Purine biosynthesis; Ligase; Lyase;
 KW Decarboxylase.
 FT DOMAIN 1 261 SAICAR SYNTHETASE.
 FT DOMAIN 262 426 AIR CARBOXYLASE.
 SQ SEQUENCE 426 AA; 47240 MW; B4A990AEB2AD360C CRC64;
 Query Match 34.1%; Score 42; DB 1; Length 426;
 Best Local Similarity 46.2%; Pred. No. 47;
 Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 QY 4 ASCHFGPLTWCK 16
 | : ||| | : |||
 Db 90 AHCEMPIEWVCR 102
 RESULT 32
 PIV2_ADECR
 ID PIV2_ADECR STANDARD; PRT; 502 AA.
 AC Q96680;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Maturation protein (Protein IVA2).
 GN PIVA2.
 OS Canine adenovirus type 1 (strain RI261).
 OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
 CC NCBI_TaxID=69151;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97275900; PubMed=9129661;
 RA Morrison M.D., Onions D.E., Nicolson L.;
 RT "Complete DNA sequence of canine adenovirus type 1."
 RL J. Gen. Virol. 78:873-878(1997).
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CC -----
DR EMBL; YC7760; CAA69056.1; -
DR InterPro; IPR003389; Adeno_IVa2.
DR Pfam; PF02456; Adeno_IVa2; 1.
KW ATP-binding. 226 233 ATP (POTENTIAL).
FT NP_BIND 502 AA; 56819 MW; 46F73C5789A0DAEA CRC64;
SQ SEQUENCE 502 AA; 56819 MW; 46F73C5789A0DAEA CRC64;

Query Match 34.1%; Score 42; DB 1; Length 502;
Best Local Similarity 36.0%; Pred. No. 54;
Matches 9; Conservative 2; Mismatches 8; Indels 6; Gaps 1;

QY 2 GTASCHFGPL-----TWVCKPQGG 20
Db 38 GKRSCHLHPLLRCAKGLLLCRPAAG 62

RESULT 33
PRLR_HUMAN STANDARD; PRT; 622 AA.
AC P16471; Q9BX87;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Prolactin receptor precursor (PRL-R).
GN PRLR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=90114212; PubMed=2558309;
RA Boutin J.-M., Edery M., Shirota M., Jolicœur C., Lesueur L.,
RA Ali S., Gould D., Djiane J., Kelly P.A.;
RT "Identification of a cDNA encoding a long form of prolactin receptor
RT in human hepatoma and breast cancer cells.";
RL Mol. Endocrinol. 3:1455-1461(1989).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=99182102; PubMed=10084611;
RA Hu Z.-Z., Zhuang L., Meng J., Leonidires M., Dufau M.;
RT "The human prolactin receptor gene structure and alternative promoter
RT utilization: the generic promoter hPRL1 and a novel human promoter
RT hP(N).";
RL J. Clin. Endocrinol. Metab. 84:1153-1156(1999).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Breast carcinoma;
RA Kline J.B., Clevenger C.V.;
RT "Characterization of a novel and functional human prolactin receptor
RT isoform (delta-S1 PRLr) containing only one extracellular
RT fibronectin-like domain.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 25-235.
RX MEDLINE=95075462; PubMed=7984244;
RA Somers W., Ultsch M., de Vos A.M., Kossiakoff A.A.;
RT "The X-ray structure of a growth hormone-prolactin receptor complex.";
RL Nature 372:478-481(1994).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
CC PROLACTIN.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC isoId=P16471-1; Sequence=Displayed;
```

```
CC Name=2; Synonyms=Delta-S1;
CC isoId=P16471-2; Sequence=VSP_001720;
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -!- SIMILARITY: Contains 2 fibronectin type III domains.
CC -----
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CC -----
DR EMBL; M31661; AAA60174.1; -
DR EMBL; AF091870; AAD32032.1; -
DR EMBL; AF091863; AAD32032.1; JOINED.
DR EMBL; AF091864; AAD32032.1; JOINED.
DR EMBL; AF091865; AAD32032.1; JOINED.
DR EMBL; AF091866; AAD32032.1; JOINED.
DR EMBL; AF091867; AAD32032.1; JOINED.
DR EMBL; AF091868; AAD32032.1; JOINED.
DR EMBL; AF091869; AAD32032.1; JOINED.
DR EMBL; AF349939; AAK32703.1; -
DR PIR; A40144; A40144.
DR PDB; 1BP3; 23-SEP-98.
DR Genew; HGNC:9446; PRLR.
DR MIM; 176761; -
DR GO; GO:0004925; F:prolactin receptor activity; TAS.
DR GO; GO:0007566; P:embryo implantation; TAS.
DR GO; GO:0007595; P:lactation; TAS.
DR InterPro; IPR002996; CRI1A.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003528; Hemtopoptn_L_F1.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 2.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat;
KW Alternative splicing; 3D-structure.
FT SIGNAL 1 24
FT CHAIN 25 622 PROLACTIN RECEPTOR.
FT DOMAIN 25 234 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 235 258 POTENTIAL.
FT DOMAIN 259 622 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 25 122 FIBRONECTIN TYPE-III 1.
FT DOMAIN 123 227 FIBRONECTIN TYPE-III 2.
FT DISULFID 36 46 BY SIMILARITY.
FT DISULFID 75 86 BY SIMILARITY.
FT CARBOHYD 59 59 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 104 104 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 233 233 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPIC 24 124 Missing (in isoform 2).
FT STRAND 31 38 /FTId=VSP_001720.
FT STRAND 44 50
FT STRAND 61 66
FT STRAND 73 74
FT TURN 80 81
FT STRAND 85 88
FT TURN 91 92
FT STRAND 98 106
FT STRAND 112 113
FT STRAND 117 120
FT HELIX 121 123
FT STRAND 125 125
FT STRAND 134 134
FT STRAND 138 138
FT STRAND 146 146
FT STRAND 149 150
FT TURN 155 156
FT TURN 159 162
FT STRAND 166 174
FT STRAND 181 186
FT TURN 187 187
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FT STRAND 190 191
FT TURN 198 199
FT STRAND 201 210
FT TURN 211 212
FT STRAND 224 225
SQ SEQUENCE 622 AA; 69505 MW; DB7FD0328608C787 CRC64;

Query Match 34.1%; Score 42; DB 1; Length 622;
Best Local Similarity 77.8%; Pred. No. 66;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGTASCHFG 9
DB 81 GGPNSCHFG 89

RESULT 34
Y115 METJA STANDARD; PRT; 155 AA.
AC Q57579;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MJ0115.
GN MJ0115.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_TaxID=2190;
RN 1;
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=868087;
RA Sult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.L.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodex A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii."
RL Science 273:1058-1073(1996).
CC -----
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```

```
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-NOV-1990 (Rel. 16, Last annotation update)
DE Hypothetical 38.4 kDa protein (ORF10).
OS Clostridium perfringens.
OG Plasmid pIP404.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1502;
RN 1;
RP SEQUENCE FROM N.A.
RC STRAIN=CPN50;
RX MEDLINE=88336297; PubMed=2901769;
RA Garnier T., Cole S.T.;
RT "Complete nucleotide sequence and genetic organization of the
RT bacteriocinogenic plasmid, pIP404, from Clostridium perfringens.";
RL Plasmid 19:134-150(1988).
CC -!- SIMILARITY: To C.perfringens CPE1502.
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```

```
EMBL; M32882; AAA98256.1; -
PIR; JT0370; JT0370.
InterPro; IPR002509; Amidase_3.
Pfam; PF01520; Amidase_3; 1.
SMART; SM00646; Ami_3; 1.
Hypothetical protein; Plasmid.
SEQUENCE 342 AA; 38364 MW; BA9BBFCAE8EB135 CRC64;

Query Match 33.7%; Score 41.5; DB 1; Length 342;
Best Local Similarity 42.3%; Pred. No. 45;
Matches 11; Conservative 1; Mismatches 3; Indels 11; Gaps 2;

QY 5 SCHF-----GPJ---TWVCKPQG 19
DB 75 SHFDKCYDKFDGPIGTGTWVCKEGG 100
```

```
RESULT 36
HIC1 MOUSE
ID HIC1 MOUSE STANDARD; PRT; 892 AA.
AC Q9R1Y5; Q9R1Y6; Q9R2B0;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Hypermethylated in cancer 1 protein (Hic-1).
GN HIC1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 1;
RP SEQUENCE FROM N.A., AND DEVELOPMENTAL STAGE.
RC STRAIN=129/Sv, and Swiss Webster; TISSUE=Embryo;
RX MEDLINE=99172081; PubMed=10072440;
RA Grimm C., Spoerle R., Schmid T.E., Adler I.-D., Adamski J.,
RA Schughart K., Graw J.;
RT "Isolation and embryonic expression of the novel mouse gene Hic1, the
RT homologue of HIC1, a candidate gene for the Miller-Dieker syndrome.";
RL Hum. Mol. Genet. 8:697-710(1999).
RN [2]
RP SEQUENCE FROM N.A., DISEASE, AND TISSUE SPECIFICITY.
RX MEDLINE=20122251; PubMed=10655551;
RA Carter M.G., Johns M.A., Zeng X., Zhou L., Zink M.C., Mankowski J.L.,
RA Donovan D.M., Baylin S.B.;
RT "Mice deficient in the candidate tumor suppressor gene Hic1 exhibit
RT developmental defects of structures affected in the Miller-Dieker
RT syndrome.";
```



```
Db 225 CNYGPGTRYAWTVLPQG 241
RESULT 38
VGLM_HANTB
ID VGLM_HANTB STANDARD; PRT; 1133 AA.
AC P28728;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE M polyprotein precursor [Contains: Glycoprotein G1; Glycoprotein G2].
GN M.
OS Hantaan virus (strain B-1) (Korean hemorrhagic fever virus).
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Hantavirus.
OX NCBI_TaxID=31617;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90370499; PubMed=2118626;
RA Isegawa Y., Fujiwara Y., Ohshima A., Fukunaga R., Murakami H.,
RA Yamaniishi K., Sokawa Y.;
RT "Nucleotide sequence of the M genome segment of hemorrhagic fever
RT with renal syndrome virus strain B-1."
RL Nucleic Acids Res. 18:4936-4936(1990).
CC -!- PTM: SPECIFIC ENZYMAIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS
CC INCLUDING GLYCOPROTEIN G1 AND GLYCOPROTEIN G2.
CC -!- SIMILARITY: BELONGS TO THE HANTAVIRUSES M POLYPROTEIN FAMILY.
CC
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CC
CC EMBL; X53861; CAA37854.1; -.
DR PIR; S12597;
DR InterPro; IPR002534; Hanta_G1.
DR InterPro; IPR002532; Hanta_G2.
DR InterPro; IPR007097; Znf_C2H2.
DR Pfam; PF01567; Hanta_G1; 1.
DR Pfam; PF01561; Hanta_G2; 1.
DR ProDom; PD001813; Hanta_G2; 1.
DR Polyprotein; Glycoprotein; Transmembrane; Nonstructural protein;
KW Signal.
FT SIGNAL 1 16 POTENTIAL.
FT CHAIN 17 1133 M POLYPROTEIN.
FT CHAIN 17 646 GLYCOPROTEIN G1.
FT CHAIN 647 1133 GLYCOPROTEIN G2.
FT CARBOHYD 132 132 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 233 233 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 345 345 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 397 397 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 560 560 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 926 926 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 1133 AA; 125908 MW; 0A25160A32862FD6 CRC64;
Query Match 33.7%; Score 41.5; DB 1; Length 1133;
Best Local Similarity 40.0%; Pred. No. 1.4e+02;
Matches 8; Conservative 1; Mismatches 6; Indels 5; Gaps 1;
QY 3 TASCHFG-----PLTWVCKP 17
DB 746 TAKCHFEDYEYENSWACNP 765
RESULT 39
VGLM_SEOU8
ID VGLM_SEOU8 STANDARD; PRT; 1133 AA.
AC P33455;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
NT 01-FEB-1994 (Rel. 28, Last sequence update)
Db 225 CNYGPGTRYAWTVLPQG 241
RESULT 38
VGLM_HANTB
ID VGLM_HANTB STANDARD; PRT; 1133 AA.
AC P28728;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE M polyprotein precursor [Contains: Glycoprotein G1; Glycoprotein G2].
GN M.
OS Hantaan virus (strain B-1) (Korean hemorrhagic fever virus).
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Hantavirus.
OX NCBI_TaxID=31617;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90370499; PubMed=2118626;
RA Isegawa Y., Fujiwara Y., Ohshima A., Fukunaga R., Murakami H.,
RA Yamaniishi K., Sokawa Y.;
RT "Nucleotide sequence of the M genome segment of hemorrhagic fever
RT with renal syndrome virus strain B-1."
RL Nucleic Acids Res. 18:4936-4936(1990).
CC -!- PTM: SPECIFIC ENZYMAIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS
CC INCLUDING GLYCOPROTEIN G1 AND GLYCOPROTEIN G2.
CC -!- SIMILARITY: BELONGS TO THE HANTAVIRUSES M POLYPROTEIN FAMILY.
CC
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CC
CC EMBL; X53861; CAA37854.1; -.
DR PIR; S12597;
DR InterPro; IPR002534; Hanta_G1.
DR InterPro; IPR002532; Hanta_G2.
DR InterPro; IPR007097; Znf_C2H2.
DR Pfam; PF01567; Hanta_G1; 1.
DR Pfam; PF01561; Hanta_G2; 1.
DR ProDom; PD001813; Hanta_G2; 1.
DR Polyprotein; Glycoprotein; Transmembrane; Nonstructural protein;
KW Signal.
FT SIGNAL 1 16 POTENTIAL.
FT CHAIN 17 1133 M POLYPROTEIN.
FT CHAIN 17 646 GLYCOPROTEIN G1.
FT CHAIN 647 1133 GLYCOPROTEIN G2.
FT CARBOHYD 132 132 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 233 233 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 345 345 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 397 397 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 560 560 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 926 926 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 1133 AA; 125908 MW; 0A25160A32862FD6 CRC64;
Query Match 33.7%; Score 41.5; DB 1; Length 1133;
Best Local Similarity 40.0%; Pred. No. 1.4e+02;
Matches 8; Conservative 1; Mismatches 6; Indels 5; Gaps 1;
QY 3 TASCHFG-----PLTWVCKP 17
DB 746 TAKCHFEDYEYENSWACNP 765
RESULT 40
VGLM_SEOUS
ID VGLM_SEOUS STANDARD; PRT; 1133 AA.
AC P17880;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE M polyprotein precursor [Contains: Glycoprotein G1; Glycoprotein G2].
GN M.
OS Seoul virus (strain SR-11) (Sapporo rat virus).
```

OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Hantavirus.
OX NCBI_TaxID=11610;

RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 17-23 AND 647-654.

RX MEDLINES=90232720; PubMed=1970443;

RA Arikawa J., Lapenotiere H.F., Iacono-Connors L., Wang M.,

RA Schmaljohn C.S.;

RT "Coding properties of the S and the M genome segments of Sapporo rat
RT virus: comparison to other causative agents of hemorrhagic fever with
RT renal syndrome.";

RL Virology 176:114-125(1990).

CC -!- PTM: SPECIFIC ENZYMOLOGICAL CLEAVAGES IN VIVO YIELD MATURE PROTEINS
CC INCLUDING GLYCOPROTEIN G1 AND GLYCOPROTEIN G2.

CC -!- SIMILARITY: BELONGS TO THE HANTAVIRUSES M POLYPROTEIN FAMILY.

CC -----
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CC -----

DR EMBL; M34882; AAA47825.1; -

DR InterPro; IPR002534; Hanta_G1.

DR InterPro; IPR002532; Hanta_G2.

DR InterPro; IPR007087; Znf_C2H2.

DR Pfam; PF01567; Hanta_G1; 1.

DR Pfam; PF01561; Hanta_G2; 1.

DR Pfam; PF00096; zf-C2H2; 1.

DR ProDom; PD001813; Hanta_G2; 1.

KW Polyprotein; Glycoprotein; Transmembrane; Signal.

FT SIGNAL 1 16 POTENTIAL.

FT CHAIN 17 1133 M POLYPROTEIN.

FT CHAIN 17 646 GLYCOPROTEIN G1.

FT CHAIN 647 1133 GLYCOPROTEIN G2.

FT TRANSMEM 444 461 POTENTIAL.

FT TRANSMEM 485 504 POTENTIAL.

FT TRANSMEM 625 646 POTENTIAL.

FT TRANSMEM 1105 1124 POTENTIAL.

FT CARBOHYD 132 132 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 233 233 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 345 345 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 397 397 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 560 560 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 926 926 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 1133 AA; 125591 MW; 8120721933AGAE5B CRC64;

SQ SEQUENCE 1133 AA; 125591 MW; 8120721933AGAE5B CRC64;

Query Match 33.7%; Score 41.5; DB 1; Length 1133;

Best Local Similarity 40.0%; Pred. No. 1.4e+02;

Matches 8; Conservative 1; Mismatches 6; Indels 5; Gaps 1;

QY 3 TASCHFG-----PLTWVCKP 17

Db 746 TAKCHFEXDYEYENSWACNP 765

||||| :|||

RESULT 41

VGLM_SEOUR

ID VGLM_SEOUR STANDARD; PRT; 1134 AA.

AC P28729;

DT 01-DEC-1992 (Rel. 24, Created)

DT 01-DEC-1992 (Rel. 24, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE M polyprotein precursor [Contains: Nonstructural protein NS-M;

DE Glycoprotein G1; Glycoprotein G2].

GN M.

CS Seoul virus (strain R22).

OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Hantavirus.

OX NCBI_TaxID=31620;

RN [1]

RP SEQUENCE FROM N.A.

RA Shi L.C., Hang C.S., Li D.X., Yuan J.S., Jin D.Y., Song G.;

RT "Molecular cloning and sequencing of the M genome segment of epidemic
RT hemorrhagic fever virus R22 strain.";

RL Ping Tu Hsueh Pao 7:295-302(1991).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=92074322; PubMed=1962503;

RA Xu X.A., Ruo S.L., Tang Y.W., Fisher-Hoch S.P., McCormick J.B.;

RT "Molecular characterization and expression of glycoprotein gene of
RT Hantavirus R22 strain isolated from Rattus norvegicus in China.";

RL Virus Res. 21:35-52(1991).

CC -!- PTM: SPECIFIC ENZYMOLOGICAL CLEAVAGES IN VIVO YIELD MATURE PROTEINS

CC INCLUDING GLYCOPROTEIN G1 AND GLYCOPROTEIN G2.

CC -!- SIMILARITY: BELONGS TO THE HANTAVIRUSES M POLYPROTEIN FAMILY.

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CC -----

DR EMBL; S68035; AAB20470.2; -

DR PIR; JCI006; GNVU22.

DR InterPro; IPR002534; Hanta_G1.

DR InterPro; IPR002532; Hanta_G2.

DR Pfam; PF01567; Hanta_G1; 1.

DR Pfam; PF01561; Hanta_G2; 1.

DR ProDom; PD001813; Hanta_G2; 1.

KW Polyprotein; Glycoprotein; Transmembrane; Nonstructural protein;

Signal.

FT SIGNAL 1 16 POTENTIAL.

FT CHAIN 17 1134 M POLYPROTEIN.

FT CHAIN 17 646 GLYCOPROTEIN G1.

FT CHAIN 647 1134 GLYCOPROTEIN G2.

FT TRANSMEM 444 461 POTENTIAL.

FT TRANSMEM 485 504 POTENTIAL.

FT TRANSMEM 625 646 POTENTIAL.

FT TRANSMEM 1106 1125 POTENTIAL.

FT CARBOHYD 132 132 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 233 233 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 345 345 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 397 397 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 560 560 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 927 927 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 285 287 EEI -> KKF (IN REF. 2).

FT CONFLICT 645 645 S -> T (IN REF. 2).

FT CONFLICT 874 874 V -> D (IN REF. 2).

SQ SEQUENCE 1134 AA; 126319 MW; 60F4918FC42EE3ED CRC64;

Query Match 33.7%; Score 41.5; DB 1; Length 1134;

Best Local Similarity 40.0%; Pred. No. 1.4e+02;

Matches 8; Conservative 1; Mismatches 6; Indels 5; Gaps 1;

QY 3 TASCHFG-----PLTWVCKP 17

Db 747 TAKCHFEXDYEYENSWACNP 766

||||| :|||

RESULT 42

UNG_CHLMU

ID UNG_CHLMU STANDARD; PRT; 229 AA.

AC Q9PJD2;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Uracil-DNA glycosylase (EC 3.2.2.-) (UDG).

GN UNG OR TC0897.

OS Chlamydia muridarum.

OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.

OX NCBI_TaxID=83560;

RN [1]

RP SEQUENCE FROM N.A.

```
RC STRAIN=MoPn / Ni99; PubMed=10684935;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
RA Gwinn M., Nelson W., DeBoy R., Kolonay G., McClarty G., Salzberg S.L.,
RA Eisen J., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
RT pneumoniae AR39.";
RJ Nucleic Acids Res. 28:1397-1406(2000).
CC -!- FUNCTION: Excises uracil residues from the DNA which can arise as
CC a result of misincorporation of dUMP residues by DNA polymerase or
CC due to deamination of cytosine (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: BELONGS TO THE URACIL-DNA GLYCOSYLASE FAMILY.
CC -----
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CC -----
CC EMBL; AE002356; AAF39691.1; ..
DR PIR; B81652; B81652.
DR HSSP; P12295; 1EUG.
DR TIGR; TC0897; ..
DR HAMAP; MF_00148; -; 1.
DR InterPro; IPR003249; U_glycsylse_notp.
DR InterPro; IPR002043; UDNA_glycsylse.
DR InterPro; IPR005122; UDNA_glycsylseSF.
DR Pfam; PF03167; UDG; 1.
DR ProDom; PD001589; U_glycsylse_notp; 1.
DR TIGRFAMs; TIGR00628; ung; 1.
DR PROSITE; PS00130; U_DNA_GLYCOSYLASE; 1.
DR DNA repair; Hydrolase; Glycosidase; Complete proteome.
KW ACT_SITE 70 70 GENERAL BASE (BY SIMILARITY).
FT ACT_SITE 229 AA; 25972 MW; C68786E753D9CA CRC64;
SQ SEQUENCE 229 AA; 25972 MW; 25972 MW; C68786E753D9CA CRC64;
-----
Query Match 33.3%; Score 41; DB 1; Length 229;
Best Local Similarity 42.9%; Pred. No. 37;
Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
QY 6 CHFGPLTWCKPQG 19
||| : : : |||
DB 207 CHFSKINYLLKKQG 220
-----
RESULT 43
UNG_CHLTR STANDARD; PRT; 229 AA.
AC 084613;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Uracil-DNA glycosylase (EC 3.2.2.-) (UDG).
GN UNG CR CT607.
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN {1}
RP SEQUENCE FROM N.A.
RC STRAIN=D/UW-3/Cx;
RX MEDLINE=99000809; PubMed=97841136;
RA Stephens R.S., Kalman S., Lammel C.C., Fan J., Marathe R., Aravind L.,
RA Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
RA Davis R.W.;
RT "Genome sequence of an obligate intracellular pathogen of humans:
RT Chlamydia trachomatis.";
RL Science 282:754-759(1998).
CC -!- FUNCTION: Excises uracil residues from the DNA which can arise as
CC a result of misincorporation of dUMP residues by DNA polymerase or
```

```
CC due to deamination of cytosine (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: BELONGS TO THE URACIL-DNA GLYCOSYLASE FAMILY.
CC -----
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CC -----
CC EMBL; AE001331; AAC68210.1; ..
DR PIR; C71493; C71493.
DR HSSP; P12295; 1EUG.
DR HAMAP; MF_00148; -; 1.
DR InterPro; IPR003249; U_glycsylse_notp.
DR InterPro; IPR002043; UDNA_glycsylse.
DR InterPro; IPR005122; UDNA_glycsylseSF.
DR Pfam; PF03167; UDG; 1.
DR ProDom; PD001589; U_glycsylse_notp; 1.
DR TIGRFAMs; TIGR00628; ung; 1.
DR PROSITE; PS00130; U_DNA_GLYCOSYLASE; 1.
DR DNA repair; Hydrolase; Glycosidase; Complete proteome.
KW ACT_SITE 70 70 GENERAL BASE (BY SIMILARITY).
FT ACT_SITE 229 AA; 26002 MW; 9AD49846F8DCDC3B CRC64;
SQ SEQUENCE 229 AA; 26002 MW; 9AD49846F8DCDC3B CRC64;
-----
Query Match 33.3%; Score 41; DB 1; Length 229;
Best Local Similarity 42.9%; Pred. No. 37;
Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
QY 6 CHFGPLTWCKPQG 19
||| : : : |||
DB 207 CHFSKINYLLKKQG 220
-----
RESULT 44
RNC_NEIMA STANDARD; PRT; 239 AA.
AC Q9JVD3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ribonuclease III (EC 3.1.26.3) (RNase III).
GN RNC OR NMA0888.
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699;
RN {1}
RP SEQUENCE FROM N.A.
RC STRAIN=22491 / Serogroup A / Serotype 4A;
RX MEDLINE=20222556; PubMed=10761919;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
RA Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,
RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrell B.G.;
RT "Complete DNA sequence of a serogroup A strain of Neisseria
RT meningitidis 22491.";
RL Nature 404:502-506(2000).
CC -!- FUNCTION: Digests double-stranded RNA. Involved in the processing
CC of ribosomal RNA precursors and of some mRNAs (By similarity).
CC -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
CC phosphomonoester.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Contains 1 DRBM (double-stranded RNA-binding) domain.
CC -!- SIMILARITY: Contains 1 RNase III domain.
CC -----
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CC -----
CC EMBL; AL162754; CAB84168.1; -.
CC PIR; C81935; C81935.
CC HAMAP; MF_00104; -.
CC InterPro; IPR001159; DS_RBD.
CC InterPro; IPR000999; RNase_3.
CC Pfam; PF00035; dsrm; 1.
CC Pfam; PF00636; Ribonuclease_3; 1.
CC SMART; SM00358; DSRM; 1.
CC SMART; SM00535; RIBOC; 1.
CC PROSITE; PS0137; DS_RBD; 1.
CC PROSITE; PS00517; RNase_3_1; FALSE_NEG.
CC PROSITE; PS0142; RNase_3_2; 1.
KW Hydrolase; Nuclease; Endonuclease; RNA-binding; Complete proteome.
FT DOMAIN 11 133 RNase III.
FT DOMAIN 160 230 DRBM.
SQ SEQUENCE 239 AA; 26841 MW; E8772B870A940CDF CRC64;

Query Match 33.3%; Score 41; DB 1; Length 239;
Best Local Similarity 46.7%; Pred. No. 39;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 5 SCHFGPLTWCKPQG 19
Db 196 SCDLGLGELGFCRAKG 210

RESULT 45
RNC_NEIMB STANDARD; PRT; 239 AA.
AC Q9KGC8;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ribonuclease III (EC 3.1.26.3) (RNase III).
GN RNC OR NYB0686.
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58 / Serogroup B;
RX MEDLINE=20175755; PubMed=10710307;
RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
RA Nelson W.C., Winn M.L., DeBoy R., Peterson J.D., Hickey E.K.,
RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
RA Mason T., Ciecko A., Parksey D.S., Blair E., Citterone H., Clark E.B.,
RA Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,
RA Gill J., Scarlato V., Maignani V., Pizzi M., Grandi G., Sun L.,
RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
RT MC58.";
RL Science 287:1809-1815(2000).
CC -!- FUNCTION: Digests double-stranded RNA. Involved in the processing
CC of ribosomal RNA precursors and of some mRNAs (By similarity).
CC -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
CC phosphomonoester.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Contains 1 DRBM (double-stranded RNA-binding) domain.
CC -!- SIMILARITY: Contains 1 RNase III domain.
CC -----
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CC -----
CC EMBL; AE002423; AAF41104.1; -.
CC PIR; E81169; E81169.
CC TIGR; NMB0686; -.
CC HAMAP; MF_00104; -.
CC InterPro; IPR001159; DS_RBD.
CC InterPro; IPR000999; RNase_3.
CC Pfam; PF00035; dsrm; 1.
CC Pfam; PF00636; Ribonuclease_3; 1.
CC SMART; SM00358; DSRM; 1.
CC SMART; SM00535; RIBOC; 1.
CC PROSITE; PS0137; DS_RBD; 1.
CC PROSITE; PS00517; RNase_3_1; FALSE_NEG.
CC PROSITE; PS0142; RNase_3_2; 1.
KW Hydrolase; Nuclease; Endonuclease; RNA-binding; Complete proteome.
FT DOMAIN 11 133 RNase III.
FT DOMAIN 160 230 DRBM.
SQ SEQUENCE 239 AA; 26853 MW; 54D0F0473049607C CRC64;

Query Match 33.3%; Score 41; DB 1; Length 239;
Best Local Similarity 46.7%; Pred. No. 39;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 5 SCHFGPLTWCKPQG 19
Db 196 SCDLGLGELGFCRAKG 210

RESULT 46
NADE_MYCGE STANDARD; PRT; 248 AA.
AC P47623;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Probable NH(3)-dependent NAD(+) synthetase (EC 6.3.5.1).
GN NADE OR MG383.
OS Mycoplasma genitalium.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33530 / G-37;
RX MEDLINE=96026346; PubMed=7569993;
RA Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
RA Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
RA Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,
RA Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,
RA Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,
RA Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
RT "The minimal gene complement of Mycoplasma genitalium.";
RL Science 270:397-403(1995).
CC -!- CATALYTIC ACTIVITY: ATP + deamido-NAD(+) + NH(3) + H(2)O = AMP +
CC diphosphate + NAD(+).
CC -!- PATHWAY: NAD biosynthesis.
CC -!- SIMILARITY: BELONGS TO THE NAD SYNTHETASE FAMILY.
CC -----
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CC -----
CC EMBL; U39720; AAC71610.1; -.
CC PIR; D64242; D64242.
CC HSSP; P08164; 2NSY.
CC TIGR; MG383; -.
CC HAMAP; MF_00193; -.
CC InterPro; IPR003694; NAD_synthase.
CC Pfam; PF02540; NAD_synthase; 1.

```

DR TIGRFAMS; TIGR00552; nadE; 1.
KW Ligase; NAD; ATP-binding; Complete proteome.
FT NP BIND 30 37 ATP (BY SIMILARITY).
FT ACT_SITE 32 32 BY SIMILARITY.
SQ SEQUENCE 248 AA; 28189 MW; 45E4BC687545220E CRC64;

Query Match 33.3%; Score 41; DB 1; Length 248;
Best Local Similarity 40.0%; Pred. No. 40;
Matches 6; Conservative 2; Mismatches 7; Indels 3; Gaps 0;

QY 2 GTASCHFGPLTWCK 16
| : | | | : |
DB 149 GDGACDIAPLAWLLK 163

RESULT 47
CYCG RHGSH STANDARD; PRT; 296 AA.
AC Q53143;
DT 01-NOV-1997 (Rel. 35, Created);
DT 01-NOV-1997 (Rel. 35, Last sequence update);
DT 28-FEB-2003 (Rel. 41, Last annotation update);
DE Diheme cytochrome C-type.
GN CYCG.
OS Rhodobacter sphaeroides (Rhodospseudomonas sphaeroides);
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
OC Rhodobacteraceae; Rhodobacter.
OX NCBI_TaxID=1063;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158;
RX MEDLINE=95362655; PubMed=7543472;
RA Flory J.E., Donohue T.J.;
RT "Organization and expression of the Rhodobacter sphaeroides cycFG operon";
RL J. Bacteriol. 177:4311-4320(1995).
CC -!- FUNCTION: DIHEME C-TYPE CYTOCHROME. THAT IS PARTICULARLY EXPRESSED WHEN CELLS GENERATE ENERGY VIA AEROBIC RESPIRATION.
CC -!- SUBCELLULAR LOCATION: Membrane-bound.
CC -!- PTM: BINDS TWO HEME GROUPS PER MOLECULE (POTENTIAL).
CC -!- SIMILARITY: TO ACETOBACTER ALCOHOL DEHYDROGENASE CYTOCHROME C SUBUNIT.

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DR EMBL; L36880; AAD09146.1; .
DR InterPro; IPR003088; Cyt C1.
DR InterPro; IPR003219; CytC adh.
DR InterPro; IPR000345; CytC_heme bind.
DR Pfam; PF00034; cytochrome_c_1.
DR ProDom; PD011584; CytC adh; 1.
DR PROSITE; PS00190; CYTOCHROME C; 2.
KW Electron transport; Heme; Membrane.
FT BINDING 52 52 HEME 1 (COVALENT) (BY SIMILARITY).
FT BINDING 55 55 HEME 1 (COVALENT) (BY SIMILARITY).
FT METAL 56 56 IRON (HEME 1 AXIAL LIGAND) (BY SIMILARITY).
FT BINDING 202 202 HEME 2 (COVALENT) (BY SIMILARITY).
FT BINDING 205 205 HEME 2 (COVALENT) (BY SIMILARITY).
FT METAL 206 206 IRON (HEME 2 AXIAL LIGAND) (BY SIMILARITY).
SQ SEQUENCE 296 AA; 31727 MW; 4C4A9D8F695858BFD CRC64;

Query Match 33.3%; Score 41; DB 1; Length 296;
Best Local Similarity 70.0%; Pred. No. 47;
Matches 7; Conservative 0; Mismatches 3; Indels 3; Gaps 0;

QY 1 GGTASCHFGP 10
| | | | | |
DB 50 GGCASCHAAP 59

RESULT 48
TLX1_HUMAN STANDARD; PRT; 330 AA.
ID TLX1_HUMAN
AC P31314; O75699; Q9HCA0;
DT 01-JUL-1993 (Rel. 26, Created);
DT 01-JUL-1993 (Rel. 26, Last sequence update);
DT 28-FEB-2003 (Rel. 41, Last annotation update);
DE T-cell leukemia homeobox protein 1 (Homeobox protein Hox-11) (TCL-3 proto-oncogene).
DE TLX1 OR HOX11 OR TCL3.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92020958; PubMed=1681546;
RA Kennedy M.A., Gonzalez-Sarmiento R., Kees U.R., Lampert F., Dear T.N., Boehm T., Rabbitts T.H.;
RT "HOX11, a homeobox-containing T-cell oncogene on human chromosome 10q24";
RL Proc. Natl. Acad. Sci. U.S.A. 88:8900-8904(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92007734; PubMed=1717256;
RA Lu M., Gong Z., Shen W., Ho A.D.;
RT "The tcl-3 proto-oncogene altered by chromosomal translocation in T-cell leukemia codes for a homeobox protein";
RL EMBO J. 10:2905-2910(1991).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=92319541; PubMed=1352396;
RA Lu M., Zhang N., Ho A.D.;
RT "Genomic organization of the putative human homeobox proto-oncogene HOX-11 (TCL-3) and its endogenous expression in T cells";
RL Oncogene 7:1325-1330(1992).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=91289163; PubMed=1676542;
RA Hatanoglu M., Roberts C.W., Minden M., Crist W.M., Korsmeyer S.J.;
RT "Derivation of a homeobox gene, HOX11, by the t(10;14) in T cell leukemia";
RL Science 253:79-82(1991).
RN [5]
RP SEQUENCE FROM N.A.
RA Watt P.M., Ranford P.R., Kees U.R.;
RT "HUG-1: a novel upstream gene neighboring HOX11 at 10q24 is expressed in a T-cell leukaemia cell line";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE OF 1-64 FROM N.A.
RX MEDLINE=98449474; PubMed=9778044;
RA Brake R.L., Kees U.R., Watt P.M.;
RT "Multiple negative elements contribute to repression of the HOX11 proto-oncogene";
RL Oncogene 17:1787-1795(1998).
CC -!- FUNCTION: CONTROLS THE GENESIS OF THE SPLEEN. BINDS TO THE DNA SEQUENCE 5-GGCGGTAAAGTG-3'.
CC -!- SUBCELLULAR LOCATION: Nuclear (probable).
CC -!- DISEASE: A FORM OF T-CELL ACUTE LYMPHOBLASTIC LEUKEMIA (T-ALL) IS CHARACTERIZED BY A CHROMOSOMAL TRANSLOCATION T(10;14)(Q24;Q11) WHICH INVOLVES HOX11 AND T-CELL RECEPTOR DELTA CHAIN (TCRD) GENES.
CC -!- SIMILARITY: Contains 1 homeobox domain.

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RT "The characterization of human ADAM15 gene structure and promoter
 RL region.";
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner J., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abranson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP INTERACTION WITH INTEGRIN ALPHA5-BETA3.
 RX MEDLINE=98184837; PubMed=9516430;
 RA Zhang X.P., Kamata T., Yokoyama K., Puzon-McLaughlin W., Takada Y.;
 RT "Specific interaction of the recombinant disintegrin-like domain of
 RI MDC-15 (metargidin, ADAM-15) with integrin alphavbeta3.";
 RJ J. Biol. Chem. 273:7345-7350(1998).
 RN [6]
 RP PHOSPHORYLATION OF TYR-715 AND TYR-735.
 RX MEDLINE=21826475; PubMed=11741929;
 RA Poghosyan Z., Robbins S.M., Houslay M.D., Webster A., Murphy G.,
 RA Edwards D.R.;
 RT "Phosphorylation-dependent interactions between ADAM15 cytoplasmic
 RL domain and Src family protein-tyrosine kinases.";
 RJ J. Biol. Chem. 277:4999-5007(2002).
 CC -!- FUNCTION: May be involved in cell-surface proteolysis, cell
 CC adhesion or intracellular protein maturation.
 CC -!- SUBUNIT: Binds 1 zinc ion per subunit (By similarity).
 CC -!- SUBUNIT: Interacts with ITAGV-ITGB3 (Vitronection receptor),
 CC PACSIN3 and SNX9. PACSIN3 and SNX9 preferentially bind the
 CC precursor but not the processed form of ADAM15, suggesting that
 CC the interaction occurs in a secretory pathway compartment prior to
 CC the medial Golgi (By similarity). Interacts specifically with Src
 CC family protein-tyrosine kinases (PTKs).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED. OVEREXPRESSED IN
 CC ARTEROSCLEROTIC LESIONS. CONSTITUTIVELY EXPRESSED IN CULTURED
 CC ENDOTHELIUM AND SMOOTH MUSCLE.
 CC -!- DOMAIN: THE CYTOPLASMIC DOMAIN INTERACTS WITH ENDOPHILIN I AND
 CC SORTING NEXIN 9 (BY SIMILARITY).
 CC -!- DOMAIN: DESINTEGRIN DOMAIN BINDS TO INTEGRIN ALPHA5-BETA3.
 CC -!- PTM: THE PRECURSOR IS CLEAVED BY A FUJIN ENDOPEPTIDASE (BY
 CC SIMILARITY).
 CC -!- PTM: Phosphorylation increases association with PTKs.
 CC -!- SIMILARITY: Belongs to peptidase family M125.
 CC -!- SIMILARITY: Contains 1 EGF-like domain.
 CC -!- SIMILARITY: Contains 1 disintegrin domain.
 CC -----
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DR EMBL; U46005; AAC51112.1; --
 DR EMBL; U41767; AAC50404.1; --
 DR EMBL; AF314227; AAM44189.1; --
 DR EMBL; BC014566; AAH14566.1; --
 DR HSSP; P18619; 1FVL.
 DR MEROPS; M12.215; --
 DR Genew; HGNC:193; ADAM15.
 DR MIM; 605548; --
 DR GO; GO:0007160; P:cell-matrix adhesion; TAS.
 DR InterPro; IPR006586; ADAM cysteine.
 DR InterPro; IPR001762; Disintegrin.
 DR InterPro; IPR006209; EGF like.
 DR InterPro; IPR001818; Matrxin.
 DR InterPro; IPR002870; Pep_M12B_propep.
 DR InterPro; IPR001590; Reprolysin.
 DR InterPro; IPR006025; Zn_MTPeptidse.
 DR Pfam; PF00200; disintegrin; 1.
 DR Pfam; PF01562; Pep_M12B_propep; 1.
 DR Pfam; PF01421; Reprolysin; 1.
 DR ProDom; PD000664; Disintegrin; 1.
 DR SMART; SMC0608; ACR; 1.
 DR SMART; SM00050; DISIN; 1.
 DR PROSITE; PS0215; ADAM_MEPRO; 1.
 DR PROSITE; PS00427; DISINTEGRIN_1; FALSE_NEG.
 DR PROSITE; PS0214; DISINTEGRIN_2; 1.
 DR PROSITE; PS00022; EGF_1; FALSE_NEG.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 DR PROSITE; PS00546; CYSTEINE_SWITCH; FALSE_NEG.
 DR Hydrolase; Metalloprotease; Zinc; Signal; Glycoprotein; Zymogen;
 KW Transmembrane; EGF-like domain; SH3-binding; Phosphorylation.
 FT SIGNAL 1 17 POTENTIAL.
 FT PROPEP 18 206 BY SIMILARITY.
 FT CHAIN 207 814 ADAM 15.
 FT DOMAIN 207 696 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 697 717 POTENTIAL.
 FT DOMAIN 718 814 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 207 414 METALLOPROTEASE.
 FT DOMAIN 421 508 DISINTEGRIN-LIKE.
 FT DOMAIN 509 656 CYS-RICH.
 FT DOMAIN 657 685 EGF-LIKE.
 FT SITE 766 772 SH3-BINDING (POTENTIAL).
 FT SITE 801 807 SH3-BINDING (POTENTIAL).
 FT SITE 179 179 CYSTEINE SWITCH (POTENTIAL).
 FT SITE 484 486 CELL ATTACHMENT SITE (POTENTIAL).
 FT METAL 348 348 ZINC (CATALYTIC) (BY SIMILARITY).
 FT ACT_SITE 349 349 BY SIMILARITY.
 FT METAL 352 352 ZINC (CATALYTIC) (BY SIMILARITY).
 FT METAL 358 358 ZINC (CATALYTIC) (BY SIMILARITY).
 FT DISULFID 323 409 POTENTIAL.
 FT DISULFID 480 493 POTENTIAL.
 FT DISULFID 657 667 BY SIMILARITY.
 FT DISULFID 661 673 BY SIMILARITY.
 FT DISULFID 675 684 BY SIMILARITY.
 FT MOD_RES 715 715 PHOSPHORYLATION.
 FT MOD_RES 735 735 PHOSPHORYLATION.
 FT CARBOHYD 237 237 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 389 389 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 606 606 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 714 714 S -> G (IN REF. 1).
 FT CONFLICT 791 791 A -> P (IN REF. 2).
 SQ SEQUENCE 814 AA; 87716 MW; 683A8368AD30996B CRC64;

Query Match 33.3%; Score 41; DB 1; Length 814;
 Best Local Similarity 37.5%; Pred. No. 1.2e+02;
 Matches 6; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

OY 5 SCHFGPLTWCKPQGG 20
 Db 470 NCQLRPSGWQCRPTRG 485

Search completed: November 5, 2003, 19:05:56
Job time : 13 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 5, 2003, 19:03:28 ; Search time 34 Seconds
(without alignments)
151.796 Million cell updates/sec

Title: US-09-863-600E-19
Perfect score: 123
Sequence: 1 GGTASCHFGPLTWVCKPQGG 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

SP:REMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50.5	41.1	155	17 Q53320	Q53320 methanobact
2	49	39.8	240	17 Q97AQ2	Q97AQ2 thermoplasm
3	49	39.8	499	3 Q02733	Q02733 saccharomyc
4	48.5	39.4	519	11 Q8BJ50	Q8BJ50 mus musculu
5	48.5	39.4	572	11 Q8BGV5	Q8BGV5 mus musculu
6	48	39.0	241	5 Q9V6U3	Q9V6U3 drosophila
7	48	39.0	852	10 Q9LI18	Q9LI18 oryza sativ
8	47	38.2	68	2 Q53375	Q53375 synechococc
9	47	38.2	209	16 Q8EJ61	Q8EJ61 shewanella
10	47	38.2	319	10 Q9M218	Q9M218 arabidopsis
11	47	38.2	324	10 Q9C5E4	Q9C5E4 arabidopsis
12	47	38.2	440	11 Q8CC47	Q8CC47 mus musculu
13	47	38.2	520	11 Q9JHK9	Q9JHK9 mus musculu
14	47	38.2	520	11 Q99KU8	Q99KU8 mus musculu
15	47	38.2	689	5 O01545	O01545 caenorhabdi
16	47	38.2	694	10 Q9FHJ8	Q9FHJ8 arabidopsis

17	47	38.2	695	10 Q9SLT7	Q9SLT7 arabidopsis
18	47	38.2	871	10 Q9LQ54	Q9LQ54 arabidopsis
19	47	38.2	2327	13 Q9IBG7	Q9IBG7 xenopus lae
20	46.5	37.8	641	11 Q8BVM2	Q8BVM2 mus musculu
21	46	37.4	94	10 Q9FQ67	Q9FQ67 helianthus
22	46	37.4	240	1 Q08710	Q08710 thermoplasm
23	46	37.4	240	17 Q9HJG6	Q9HJG6 thermoplasm
24	46	37.4	270	2 Q33722	Q33722 spirulina p
25	46	37.4	272	16 Q44502	Q44502 anabaena sp
26	46	37.4	347	5 Q45177	Q45177 caenorhabdi
27	46	37.4	1627	10 Q8GU51	Q8GU51 oryza sativ
28	45.5	37.0	256	10 Q9LT12	Q9LT12 arabidopsis
29	45.5	37.0	289	16 Q8XZ32	Q8XZ32 raietonia s
30	45.5	37.0	323	16 Q8XZ33	Q8XZ33 raietonia s
31	45.5	37.0	356	10 Q9LT13	Q9LT13 arabidopsis
32	45.5	37.0	494	4 Q95965	Q95965 homo sapien
33	45.5	37.0	494	11 Q8VDV0	Q8VDV0 mus musculu
34	45.5	37.0	548	4 Q8N172	Q8N172 homo sapien
35	45	36.6	79	12 Q8QUL9	Q8QUL9 infectious
36	45	36.6	220	16 Q8YSR8	Q8YSR8 anabaena sp
37	45	36.6	254	11 Q8K4K8	Q8K4K8 mus musculu
38	45	36.6	277	2 Q07873	Q07873 synechococc
39	45	36.6	338	10 Q8LAH5	Q8LAH5 arabidopsis
40	45	36.6	370	16 Q9RRJ7	Q9RRJ7 deinococcus
41	45	36.6	373	10 Q8LJS6	Q8LJS6 chlamydomon
42	45	36.6	534	10 Q9LGT2	Q9LGT2 oryza sativ
43	45	36.6	1225	12 Q91IE0	Q91IE0 lymantria d
44	45	36.6	1225	12 Q8B976	Q8B976 dendrolimus
45	45	36.6	1290	16 Q8YSJ3	Q8YSJ3 anabaena sp
46	45	36.6	1494	10 Q8H5A7	Q8H5A7 oryza sativ
47	45	36.6	1622	10 Q9C8G9	Q9C8G9 arabidopsis
48	45	36.6	1622	10 Q24635	Q24635 arabidopsis
49	45	36.6	2910	5 Q26008	Q26008 plasmodium
50	45	36.6	2914	5 Q8I410	Q8I410 plasmodium
51	44.5	36.2	210	11 Q8BKJ4	Q8BKJ4 mus musculu
52	44.5	36.2	494	11 Q8BMS0	Q8BMS0 mus musculu
53	44.5	36.2	1321	12 Q8BEM8	Q8BEM8 callitrichi
54	44	35.8	158	16 Q8XSV7	Q8XSV7 raietonia s
55	44	35.8	180	2 Q82968	Q82968 raietonia s
56	44	35.8	209	12 Q8QTY4	Q8QTY4 foot-and-mo
57	44	35.8	314	12 Q84584	Q84584 paramecium
58	44	35.8	338	10 Q93Y57	Q93Y57 arabidopsis
59	44	35.8	338	10 Q9LY31	Q9LY31 arabidopsis
60	44	35.8	374	2 Q8GLI2	Q8GLI2 bacillus ha
61	44	35.8	388	16 Q9KB30	Q9KB30 bacillus ha
62	44	35.8	422	4 Q8IXW4	Q8IXW4 homo sapien
63	44	35.8	435	13 Q9PUJ6	Q9PUJ6 carassius a
64	44	35.8	608	16 Q8D5U9	Q8D5U9 vibrio vuln
65	44	35.8	628	3 Q96X54	Q96X54 aspergillus
66	44	35.8	628	3 Q8NK90	Q8NK90 aspergillus
67	44	35.8	733	16 Q8U5K5	Q8U5K5 agrobacteri
68	44	35.8	1539	10 Q41813	Q41813 zea mays (m
69	43.5	35.4	482	10 Q8RV20	Q8RV20 oryza sativ
70	43.5	35.4	1284	16 Q98DC9	Q98DC9 rhizobium l
71	43	35.0	106	16 Q8NQV6	Q8NQV6 corynebacte
72	43	35.0	119	16 Q8U8S6	Q8U8S6 agrobacteri
73	43	35.0	205	12 Q8BEF8	Q8BEF8 foot-and-mo
74	43	35.0	209	12 Q8QTX5	Q8QTX5 foot-and-mo
75	43	35.0	210	12 Q8QTY2	Q8QTY2 foot-and-mo
76	43	35.0	210	12 Q8BEE8	Q8BEE8 foot-and-mo
77	43	35.0	211	12 Q8QTX2	Q8QTX2 foot-and-mo
78	43	35.0	211	12 Q8QTY0	Q8QTY0 foot-and-mo
79	43	35.0	211	12 Q8QTX9	Q8QTX9 foot-and-mo
80	43	35.0	211	12 Q9DJD3	Q9DJD3 foot-and-mo
81	43	35.0	211	12 Q8BEF5	Q8BEF5 foot-and-mo
82	43	35.0	211	12 Q8BEF1	Q8BEF1 foot-and-mo
83	43	35.0	211	12 Q8BEE1	Q8BEE1 foot-and-mo
84	43	35.0	211	12 Q8BED0	Q8BED0 foot-and-mo
85	43	35.0	211	12 Q8BEC5	Q8BEC5 foot-and-mo
86	43	35.0	211	12 Q8BEC0	Q8BEC0 foot-and-mo
87	43	35.0	211	12 Q8BEB9	Q8BEB9 foot-and-mo
88	43	35.0	211	12 Q8BEB2	Q8BEB2 foot-and-mo
89	43	35.0	211	12 Q8BEB1	Q8BEB1 foot-and-mo

90 Q8bea8 foot-and-mo
91 Q8bea6 foot-and-mo
92 P90489 kaposi's sa
93 P89322 foot-and-mo
94 Q8bmn2 mus musculu
95 Q9xuv6 caenorhabdi
96 Q8s6z8 oryza sativ
97 Q8sy38 drosophila
98 Q8bzf0 mus musculu
99 Q9er70 mus musculu
100 Q8wrq7 sus scrofa

ALIGNMENTS

RESULT 1
Q53320 PRELIMINARY; PRT; 155 AA.
AC Q53320;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update);
DE Conserved protein.
GN MTH1014.
OS Methanobacterium thermoautotrophicum.
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC Methanobacteriaceae; Methanothermobacter.
OX NCBI_TaxID=187420;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Delta H;
RX MEDLINE=98037514; PubMed=9371463;
RA Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,
Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,
Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
RT "Complete genome sequence of Methanobacterium thermoautotrophicum
deltaH: functional analysis and comparative genomics.";
RL J. Bacteriol. 179:7135-7155(1997).
EN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Delta H;
RX MEDLINE=93259970; PubMed=8491734;
RA Kuhner C.H., Lindenbach B.D., Wolfe R.S.;
RT "Component A2 of methylcoenzyme M reductase system from
Methanobacterium thermoautotrophicum delta H: nucleotide sequence and
functional expression by Escherichia coli.";
RL J. Bacteriol. 175:3195-3203(1993).
DR EMBL; AE000874; AAB85510.1; -.
DR EMBL; S61233; AAB26632.1; -.
KW Complete proteome.
SQ SEQUENCE 155 AA; 17219 MW; C692E8A8637B8359 CRC64;

Query Match 41.1%; Score 50.5; DB 17; Length 155;
Best Local Similarity 56.2%; Pred. No. 3.8;
Matches 9; Conservative 1; Mismatches 5; Indels 1; Gaps 1;

QY 2 GTASCHFGPLTWCKP 17
Db 61 GQGTC-FGSLWCKP 75

RESULT 2
Q97AQ2 PRELIMINARY; PRT; 240 AA.
ID Q97AQ2

AC Q97AQ2;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Succinate dehydrogenase iron sulfur subunit.
GN TV0757 OR TVG0761062.
OS Thermoplasma volcanium.
OC Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmales;
OC Thermoplasmataceae; Thermoplasma.
OX NCBI_TaxID=50339;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GSS1 / DSM 4299 / JCM 9571;
RX MEDLINE=20570466; PubMed=11121031;
RA Kawashima T., Amano N., Koike H., Makino S.-I., Higuchi S.,
Kawashima-Ohya Y., Watanabe K., Yamazaki M., Kanehori K., Kawamoto T.,
Nunoshiba T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.;
RT "Archaeal adaptation to higher temperatures revealed by genomic
sequence of Thermoplasma volcanium.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000).
DR EMBL; AP000993; BAB59899.1; -.
DR HSSP; P00364; IKF6.
DR InterPro; IPR001450; 4Fe4S_ferredoxin.
DR InterPro; IPR004489; DhsB.
DR InterPro; IPR001041; Ferredoxin.
DR Pfam; PF00111; fer2; 1.
DR Pfam; PF00037; fer4; 1.
DR TIGRFAMs; TIGR00384; dhsB; 1.
DR PROSITE; PS00198; 4FE4S_FERREDOXIN; 1.
KW Complete proteome.
SQ SEQUENCE 240 AA; 27281 MW; 617B049199893018 CRC64;

Query Match 39.8%; Score 49; DB 17; Length 240;
Best Local Similarity 63.2%; Pred. No. 10;
Matches 12; Conservative 1; Mismatches 4; Indels 2; Gaps 2;

QY 2 GTASCHF-GPLTWCKPQG 19
Db 198 GTARCHPAGECTEVC-PKG 215

RESULT 3
Q02733 PRELIMINARY; PRT; 499 AA.
ID Q02733
AC Q02733;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE LPB14P.
GN YPL017C OR LPB14C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85061207; PubMed=6095044;
RA Yang B., Friedberg E.C.;
RT "Molecular cloning and nucleotide sequence analysis of the
Saccharomyces cerevisiae RAD1 gene.";
RL Mol. Cell. Biol. 4:2161-2169(1984).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92357722; PubMed=1379722;
RA Stepien P.P., Margossian S.P., Landsman D., Butow R.A.;
RT "The yeast nuclear gene suv3 affecting mitochondrial post-
transcriptional processes encodes a putative ATP-dependent RNA
helicase.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:6813-6817(1992).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=95081072; PubMed=7989303;
RA Hiser L., Basson M.E., Rine J.;

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RT "ERG10 from Saccharomyces cerevisiae encodes acetoacetyl-CoA
RT thiolase.";
RL J. Biol. Chem. 269:31383-31389(1994).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=97313271; PubMed=9169875;
RA Bussey H., Storms R.K., Ahmed A., Albertmann K., Allen E., Ansoerge W.,
RA Araujo R., Aparicio A., Barrell B., Badcock K., Benes V., Botstein D.,
RA Bowman S., Bruckner M., Carpenter J., Cherry J.M., Chung E.,
RA Churcher C., Coster F., Davis K., Davis R.W., Dietrich F.S.,
RA Delius H., DiPaolo T., Dubois E., Dusterhoft A., Duncan M., Floeth M.,
RA Fortin N., Friesen J.D., Fritz C., Goffeau A., Hall J., Hebling U.,
RA Heumann K., Hilbert H., Hillier L., Hunnicke-Smith S., Hyman R.,
RA Johnston M., Kalman S., Kleine K., Komp C., Kurdi O., Lashkari D.,
RA Lew H., Lin A., Lin D., Louis E.J., Marathe R., Messenguy F.,
RA Mewes H.W., Mirtipati S., Moestl D., Muller-Auer S., Namath A.,
RA Nentwich U., Oefner P., Pearson D., Petel F.X., Pohl T.M.,
RA Purnelle D., Schafer M., Scharfe M., Scherens B., Schramm S.,
RA Schroeder M., Sdicu A.M., Tettelin H., Urrestarazu L.A., Ushinsky S.,
RA Vierendeels F., Vissers S., Voss H., Walsh S.V., Wambutt R., Wang Y.,
RA Wedler E., Wedler H., Winnett E., Zhong W.W., Zollner A., Vo D.H.,
RA Hari J.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XVI.";
RL Nature 387:0-0(0).
RN [5]
RP SEQUENCE FROM N.A.
RA Wang Y., Ahmed A., Bussey H., Fortin N., Friesen J.D., Hall J.,
RA Storms R.K., Vo D.H., Winnett E.;
RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RA Jia Y., Cherry J.M.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
CC -!- COFACTOR: FAD (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE PYRIDINE NUCLEOTIDE-DISULFIDE
CC OX:DOREDUCTASES CLASS-I.
DR EMBL; U36624; AAB68170.1; -.
DR HSSP; P18925; 3LAD.
DR SGD; S0005938; YPL017C.
DR InterPro; IPR001327; FAD_pyr_redox.
DR InterPro; IPR000815; Hg_reductase.
DR InterPro; IPR001100; Pyr_redox.
DR InterPro; IPR004099; pyr_redox_dim.
DR Pfam; PF00070; pyr_redox; 1.
DR Pfam; PF02852; Pyr_redox_dim; 1.
DR PRINTS; PR00368; FADPNR.
DR PRINTS; PR00945; HGRDTASE.
DR PRINTS; PR00411; PNDRDTASE1.
DR ProDom; PD000139; FAD_pyr_redox; 1.
KW FAD; Flavoprotein; Oxidoreductase; Redox-active center.
SQ SEQUENCE 499 AA; 54156 MW; 1EF2A29D4327031B CRC64;

Query Match 39.8%; Score 49; DB 3; Length 499;
Best Local Similarity 47.4%; Pred. No. 21;
Matches 9; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 2 GTASCHFGPLTWCKPQGG 20
DB 361 GTSNCGFPNVLVCQPQIG 379

RESULT 4
Q8BJ50
ID Q8BJ50 PRELIMINARY; PRT; 519 AA.
AC Q8BJ50;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Zinc finger protein 4 homolog.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

"ERG10 from Saccharomyces cerevisiae encodes acetoacetyl-CoA
thiolase.";
J. Biol. Chem. 269:31383-31389(1994).
[4]
SEQUENCE FROM N.A.
MEDLINE=97313271; PubMed=9169875;
Bussey H., Storms R.K., Ahmed A., Albertmann K., Allen E., Ansoerge W.,
Araujo R., Aparicio A., Barrell B., Badcock K., Benes V., Botstein D.,
Bowman S., Bruckner M., Carpenter J., Cherry J.M., Chung E.,
Churcher C., Coster F., Davis K., Davis R.W., Dietrich F.S.,
Delius H., DiPaolo T., Dubois E., Dusterhoft A., Duncan M., Floeth M.,
Fortin N., Friesen J.D., Fritz C., Goffeau A., Hall J., Hebling U.,
Heumann K., Hilbert H., Hillier L., Hunnicke-Smith S., Hyman R.,
Johnston M., Kalman S., Kleine K., Komp C., Kurdi O., Lashkari D.,
Lew H., Lin A., Lin D., Louis E.J., Marathe R., Messenguy F.,
Mewes H.W., Mirtipati S., Moestl D., Muller-Auer S., Namath A.,
Nentwich U., Oefner P., Pearson D., Petel F.X., Pohl T.M.,
Purnelle D., Schafer M., Scharfe M., Scherens B., Schramm S.,
Schroeder M., Sdicu A.M., Tettelin H., Urrestarazu L.A., Ushinsky S.,
Vierendeels F., Vissers S., Voss H., Walsh S.V., Wambutt R., Wang Y.,
Wedler E., Wedler H., Winnett E., Zhong W.W., Zollner A., Vo D.H.,
Hari J.;
"The nucleotide sequence of Saccharomyces cerevisiae chromosome XVI.";
Nature 387:0-0(0).
[5]
SEQUENCE FROM N.A.
Wang Y., Ahmed A., Bussey H., Fortin N., Friesen J.D., Hall J.,
Storms R.K., Vo D.H., Winnett E.;
Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
[6]
SEQUENCE FROM N.A.
Jia Y., Cherry J.M.;
Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
-!- COFACTOR: FAD (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE PYRIDINE NUCLEOTIDE-DISULFIDE
OX:DOREDUCTASES CLASS-I.
EMBL; U36624; AAB68170.1; -.
HSSP; P18925; 3LAD.
SGD; S0005938; YPL017C.
InterPro; IPR001327; FAD_pyr_redox.
InterPro; IPR000815; Hg_reductase.
InterPro; IPR001100; Pyr_redox.
InterPro; IPR004099; pyr_redox_dim.
Pfam; PF00070; pyr_redox; 1.
Pfam; PF02852; Pyr_redox_dim; 1.
PRINTS; PR00368; FADPNR.
PRINTS; PR00945; HGRDTASE.
PRINTS; PR00411; PNDRDTASE1.
ProDom; PD000139; FAD_pyr_redox; 1.
KW FAD; Flavoprotein; Oxidoreductase; Redox-active center.
SQ SEQUENCE 499 AA; 54156 MW; 1EF2A29D4327031B CRC64;

Query Match 39.8%; Score 49; DB 3; Length 499;
Best Local Similarity 47.4%; Pred. No. 21;
Matches 9; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 2 GTASCHFGPLTWCKPQGG 20
DB 361 GTSNCGFPNVLVCQPQIG 379

RESULT 4
Q8BJ50
ID Q8BJ50 PRELIMINARY; PRT; 519 AA.
AC Q8BJ50;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Zinc finger protein 4 homolog.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK032046; BAC27668.1; -.
SQ SEQUENCE 519 AA; 58661 MW; 034AE260772456E9 CRC64;

Query Match 39.4%; Score 48.5; DB 11; Length 519;
Best Local Similarity 44.4%; Pred. No. 26;
Matches 8; Conservative 4; Mismatches 3; Indels 3; Gaps 1;

QY 1 GGTASCHFGPLTWCKPQ 18
DB 36 GGTGACHPG--WILEPE 50

RESULT 5
Q8BGV5
ID Q8BGV5 PRELIMINARY; PRT; 572 AA.
AC Q8BGV5;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Zinc finger protein 8 (zinc finger protein 4 homolog).
GN ZNF8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CD-1;
RX MEDLINE=22257963; PubMed=12370310;
RA Jiao K., Zhou Y., Hogan B.L.M.;
RT "Identification of mZnf8, a Mouse Kruppel-Like Transcriptional
RT Repressor, as a Novel Nuclear Interaction Partner of Smad1.";
RL Mol. Cell. Biol. 22:7633-7644(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AF480861; AAN40973.1; -.
DR EMBL; AK035906; BAC29237.1; -.
SQ SEQUENCE 572 AA; 64736 MW; 6BC546057EAE5A04 CRC64;

Query Match 39.4%; Score 48.5; DB 11; Length 572;
Best Local Similarity 44.4%; Pred. No. 29;
Matches 8; Conservative 4; Mismatches 3; Indels 3; Gaps 1;

QY 1 GGTASCHFGPLTWCKPQ 18
DB 89 GGTGACHPG--WILEPE 103

RESULT 6
Q9V6U3
ID Q9V6U3 PRELIMINARY; PRT; 241 AA.
AC Q9V6U3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE CG10808 protein (RH60941p).
GN SYNAPTOGYRIN OR CG10808.

```

OS *Drosophila melanogaster* (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
CX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins K.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhakdev P., Brothier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Bolshakov S.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karp G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*."
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacle J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF003817; AAF58329.1; -;
DR EMBL: AY071753; AAL49375.1; -;
DR FlyBase: FBgn0033876; synaptogyrin.
DR InterPro: IPR004904; Synaptogyrin.
DR Pfam: PF03218; Synaptogyrin; 1.
SQ SEQUENCE 241 AA; 26610 MW; CFDBA1D44450E86A CRC64;

Query Match 39.0%; Score 48; DB 5; Length 241;
Best Local Similarity 55.6%; Pred. No. 14;
Matches 10; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQ 18
||| | | | | | | | | |
Db 18 GKGAGGAFDPLTFMKPQ 35

RESULT 7
Q9LI18
ID Q9LI18 PRELIMINARY; PRT; 852 AA.
AC Q9LI18;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE EST AU057816(S21817) corresponds to a region of the predicted
DE gene.
OS *Oryza sativa* (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
RT clone: P0708G02.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AP001539; BAA92920.1; -;
DR Gramene: Q9LI18; -;
DR InterPro: IPR000270; OPR_PBL.
DR InterPro: IPR003035; RWP-RK.
DR Pfam: PF00564; PBL; 1.
DR Pfam: PF02042; RWP-RK; 1.
DR SMART: SM00666; PBL; 1.
SQ SEQUENCE 852 AA; 94146 MW; 3F8512886220B970 CRC64;

Query Match 39.0%; Score 48; DB 10; Length 852;
Best Local Similarity 62.5%; Pred. No. 51;
Matches 10; Conservative 1; Mismatches 3; Indels 2; Gaps 1;

QY 4 ASCHFGPL--TWCKP 17
|||| | | | | |
Db 678 ASCHGSPANQTFVCKP 693

RESULT 8
Q53375
ID Q53375 PRELIMINARY; PRT; 68 AA.
AC Q53375;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE URF 10.
OS *Synechococcus* sp. (strain PCC 6716).
OC Bacteria; Cyanobacteria; Chroococcales; *Synechococcus*.
OX NCBI_TaxID=32048;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=6716;
RX MEDLINE=93371369; PubMed=8363578;
RA van Walraven H.S., Lutter R., Walker J.E.;
RT "Organization and sequences of genes for the subunits of ATP synthase
RT in the thermophilic cyanobacterium *Synechococcus* 6716.";
RL Biochem. J. 294:239-251(1993).
DR EMBL: X70432; CAA49886.1; -;
FT CHAIN 2 68 POTENTIAL.
SQ SEQUENCE 68 AA; 7520 MW; 77653F6F92DCC9D9 CRC64;

Query Match 38.2%; Score 47; DB 2; Length 68;
Best Local Similarity 50.0%; Pred. No. 5.9;
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 GTASCHFGPLTWCKP 17
| | | | | | | | | |
Db 8 GNSMSMTGPTITWIKP 23

RESULT 9
Q8EJ61

```
ID Q8EJ61 PRELIMINARY; PRT; 209 AA.
AC Q8EC61;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Stringent starvation protein a.
EN SSPA OR S00611.
GN Shewanella oneidensis.
OS Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Alteromonadaceae; Shewanella.
OX NCBI_TaxID=70863;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MR-1;
RX MEDLINE=22297686; PubMed=12368813;
RA Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,
RA Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A.,
RA Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F.,
RA Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M.,
RA Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C.,
RA Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A.,
RA Feldblyum T.V., Smith H.O., Venter J.C., Nealon K.H., Fraser C.M.;
RT "Genome sequence of the dissimilatory metal ion-reducing bacterium
RT Shewanella oneidensis.";
RL Nat. Biotechnol. 20:1118-1123(2002).
DR EMBL; AE015508; AAN53689.1; -.
DR TIGR; SO0611; -.
KW Complete proteome.
SQ SEQUENCE 209 AA; 24081 MW; B6846672B8767E52 CRC64;

Query Match 38.2%; Score 47; DB 16; Length 209;
Best Local Similarity 58.3%; Pred. No. 18;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 GTASCHFGPLTW 13
   | | | | |
Db 153 GLADCYLGPLLW 164

RESULT 10
Q9M218 ID Q9M218 PRELIMINARY; PRT; 319 AA.
AC Q9M218;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Hypothetical 34.4 kDa protein.
GN T8B10.70.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Rieger M., Mueller-Auer S., Zipp M., Schaefer M., Mewes H.W.,
RA Lemcke K., Mayer K.F.X., Quetier F., Salancubat M.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL138646; CAB81827.1; -.
KW Hypothetical protein.
SQ SEQUENCE 319 AA; 34419 MW; ACAB300D6FC9707D CRC64;

Query Match 38.2%; Score 47; DB 10; Length 319;
Best Local Similarity 44.4%; Pred. No. 27;
Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQ 18
   | | | | |
Db 153 GLADCYLGPLLW 164

RESULT 10
Q9M218 ID Q9M218 PRELIMINARY; PRT; 319 AA.
AC Q9M218;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Hypothetical 34.4 kDa protein.
GN T8B10.70.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Rieger M., Mueller-Auer S., Zipp M., Schaefer M., Mewes H.W.,
RA Lemcke K., Mayer K.F.X., Quetier F., Salancubat M.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL138646; CAB81827.1; -.
KW Hypothetical protein.
SQ SEQUENCE 319 AA; 34419 MW; ACAB300D6FC9707D CRC64;
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Db 183 GGOEADFEFGPKTNLRPR 200

RESULT 11
Q9C5E4 ID Q9C5E4 PRELIMINARY; PRT; 324 AA.
AC Q9C5E4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical 35.1 kDa protein.
GN T8B10.70/AT3G60410.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
RA Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,
RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
RA Seki M., Shinn P., Southwick A., Shinzaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RT "Full Length cDNA of gene T8B10.70/AT3G60410 (GI:7287989).";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF360301; AAK26011.1; -.
KW Hypothetical protein.
FT VARIANT 47 47 P -> L.
SQ SEQUENCE 324 AA; 35053 MW; 4DADC919C11CAD8E CRC64;

Query Match 38.2%; Score 47; DB 10; Length 324;
Best Local Similarity 44.4%; Pred. No. 28;
Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQ 18
   | | | | |
Db 188 GGOEADFEFGPKTNLRPR 205

RESULT 12
Q8CC47 ID Q8CC47 PRELIMINARY; PRT; 440 AA.
AC Q8CC47;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Galactosamine.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Diencephalon;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK033946; BAC28521.1; -.
SQ SEQUENCE 440 AA; 48556 MW; A750CDS783AF02D4 CRC64;

Query Match 38.2%; Score 47; DB 11; Length 440;
Best Local Similarity 50.0%; Pred. No. 38;
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 GTASCHFGPLTWCKP 17
   | | | | |
Db 158 GSPNCHFGPYDNKAKP 173
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RESULT 13
Q9JHK9
ID Q9JHK9 PRELIMINARY; PRT; 520 AA.
AC Q9CHK9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE N-acetylglucosamine-6-sulfate sulfatase.
GN GALNS.
CS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1];
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ, and C57BL/6J;
RX MEDLINE=20164110; PubMed=10699374;
RA Montano A.M., Yamagishi A., Tomatsu S., Fukuda S., Copeland N.G.,
RA Orii K.E., Isogai K., Yamada N., Kato Z.I., Jenkins N.A.,
RA Gilbert D.J., Sukegawa K., Orii T., Kondo N.;
RT "The mouse N-acetylglucosamine-6-sulfate sulfatase (GALNS) gene:
RT cDNA isolation, genomic characterization, chromosomal assignment and
RT analysis of the 5'-flanking region.";
RL Biochim. Biophys. Acta 1500:323-334 (2000).
DR EMBL; AF112242; AAF63858.1; -.
DR EXBL; AF112230; AAF63858.1; JOINED.
DR EMBL; AF112231; AAF63858.1; JOINED.
DR EXBL; AF112232; AAF63858.1; JOINED.
DR EMBL; AF112233; AAF63858.1; JOINED.
DR EMBL; AF112234; AAF63858.1; JOINED.
DR EMBL; AF112235; AAF63858.1; JOINED.
DR EMBL; AF112236; AAF63858.1; JOINED.
DR EMBL; AF112237; AAF63858.1; JOINED.
DR EMBL; AF112238; AAF63858.1; JOINED.
DR EXBL; AF112239; AAF63858.1; JOINED.
DR EXBL; AF112240; AAF63858.1; JOINED.
DR EMBL; AF112241; AAF63858.1; JOINED.
DR EXBL; AF111346; AAF63155.1; -.
DR HSSP; P15848; IFSU.
DR MGD; MGI:1355303; Galns.
DR InterPro; IPR000917; Sulfatase.
DR Pfam; PF00884; Sulfatase; 1.
DR PROSITE; PS00523; SULFATASE_1; 1.
SQ SEQUENCE 520 AA; 57672 MW; 1F99E31A8CA3A36B CRC64;

Query Match 38.2%; Score 47; DB 11; Length 520;
Best Local Similarity 50.0%; Pred. No. 44;
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 GTASCHFGPLTWCKP 17
Db 158 GSPNCHFGPYDNKAKP 173

RESULT 14
Q99KU8
ID Q99KU8 PRELIMINARY; PRT; 520 AA.
AC Q99KU8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Similar to galactosamine (N-acetyl)-6-sulfate sulfatase.
GN GALNS.
CS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1];
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.

QY 2 GTASCHFGPLTWCKP 17
Db 158 GSPNCHFGPYDNKAKP 173

Query Match 38.2%; Score 47; DB 11; Length 520;
Best Local Similarity 50.0%; Pred. No. 44;
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 GTASCHFGPLTWCKP 17
Db 158 GSPNCHFGPYDNKAKP 173

RESULT 15
O01545
ID O01545 PRELIMINARY; PRT; 689 AA.
AC O01545;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 79.2 kDa protein.
GN F31F7.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1];
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018 (1998).
RN [2];
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Ledwith J., Wohldmann P.;
RT "The sequence of C. elegans cosmid F31F7.";
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [3];
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RT "Direct Submission.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; U97011; AAB52325.2; -.
DR WormPep; F31F7.2; CE29303.
DR InterPro; IPR02035; VWF_A.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS50234; VWF_A; 1.
KW Hypothetical protein.
SQ SEQUENCE 689 AA; 79198 MW; 42C44D9BB2D76727 CRC64;

Query Match 38.2%; Score 47; DB 5; Length 689;
Best Local Similarity 53.8%; Pred. No. 59;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 GTASCHFGPLTWV 14
Db 266 GSSSTRFGPLCWI 278

RESULT 16
Q9FHJ8
ID Q9FHJ8 PRELIMINARY; PRT; 694 AA.
AC Q9FHJ8;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
```


RA Matsui M., Mizuseki K., Nakatani J., Nakanishi S., Sasai Y.;
RT "Xenopus Kiellin: A dorsalizing factor containing multiple chordin-type
RT repeats secreted from the embryonic midline";
RL Proc. Natl. Acad. Sci. U.S.A. 97:5291-5296(2000).
DR EMBL: ASC26192; BAA95483.1; -.
DR HSSP: P56682; 1CCV.
DR InterPro: IPR006209; EGF-like.
DR InterPro: IPR002919; TIL_Cysrich.
DR InterPro: IPR003129; TSPN.
DR InterPro: IPR001007; VWF_C.
DR InterPro: IPR001846; VWF_D.
DR Pfam: PF01826; TIL; 1.
DR Pfam: PF00093; VWC; 22.
DR Pfam: PF00094; vwd; 1.
DR SMART: SM00210; TSPN; 1.
DR SMART: SM00214; VWC; 27.
DR SMART: SM00216; VWD; 1.
DR PROSITE: PS01186; EGF_2; 1.
DR PROSITE: PS01208; VWF_C; 20.
SQ SEQUENCE 2327 AA; 255800 MW; 0293109329209983 CRC64;

Query Match 38.2%; Score 47; DB 13; Length 2327;
Best Local Similarity 57.1%; Pred. No. 2e-02;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 5 SCHFGPLTWCKPQ 18
:||| |||||
Db 1823 TCHCKLTWVCVHQ 1836

RESULT 20
Q8BVM2
ID Q8BVM2 PRELIMINARY; PRT; 641 AA.
AC Q8BVM2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created);
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update);
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update);
DE Hypothetical proline-rich region/von Willebrand factor type A domain
DE containing protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10093;
"Y [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=22354683; PubMed=12466851;
RA The PANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase 1 & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573 (2002).
DR EMBL: AK077206; BAC36683.1; -.
KW Hypothetical protein.
SQ SEQUENCE 641 AA; 70415 MW; 19923007308585E3 CRC64;

Query Match 37.8%; Score 46.5; DB 11; Length 641;
Best Local Similarity 61.1%; Pred. No. 66;
Matches 11; Conservative 0; Mismatches 4; Indels 3; Gaps 2;

QY 5 SCHFGPLTWCKP--QQG 20
||| ||| ||| |||
Db 487 SCHPMPLW-CHPKAQGG 503

RESULT 21:
Q9FQ67
ID Q9FQ67 PRELIMINARY; PRT; 94 AA.
AC Q9FQ67;
DT 01-MAR-2001 (TrEMBLrel. 16, Created);
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update);
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update);
DE Resistance protein candidate RGC Ha-1B39 (Fragment).

OS Helianthus annuus (Common sunflower).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; campanulids; Asterales; Asteraceae; Asteroideae;
OC Heliantheae; Helianthus.
OX NCBI_TaxID=4232;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21239344; PubMed=11341730;
RA Gedil M.A., Slabaugh M.B., Berry S., Johnson R., Michelmore R.,
RA Miller J., Gulya T., Knapp S.J.;
RT "Candidate disease resistance genes in sunflower cloned using
RT conserved nucleotide-binding site motifs: genetic mapping and linkage
RT to the downy mildew resistance gene P11";
RL Genome 44:205-212(2001).
DR EMBL: AF272767; AAG49216.1; -.
DR InterPro: IPR002182; NB-ARC.
DR Pfam: PF00931; NB-ARC; 1.
FT NON_TER 1
FT NON_TER 94
SQ SEQUENCE 94 AA; 11174 MW; 0011912DCA83E35D CRC64;

Query Match 37.4%; Score 46; DB 10; Length 94;
Best Local Similarity 77.8%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 HFGPLTWVC 15
||| |||||
Db 14 HFEKXTWVC 22

RESULT 22
Q08710
ID Q08710 PRELIMINARY; PRT; 240 AA.
AC Q08710;
DT 01-NOV-1996 (TrEMBLrel. 01, Created);
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update);
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update);
DE Succinate dehydrogenase.
OS Thermoplasma acidophilum.
OC Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
OC Thermoplasmataceae; Thermoplasma.
OX NCBI_TaxID=2303;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=122-1B2 AMRC-914;
RX MEDLINE=93326626; PubMed=8334158;
RA Bach M., Reilaender H., Gaertner P., Lottspeich F., Michel H.;
RT "Nucleotide sequence of a putative succinate dehydrogenase operon in
RT Thermoplasma acidophilum";
RL Biochim. Biophys. Acta 1174:103-107(1993).
DR EMBL: X70908; CAA50262.1; -.
DR HSSP: P00364; 1KF6.
DR InterPro: IPR001450; 4Fe4S_ferredoxin.
DR InterPro: IPR004489; DhsB.
DR InterPro: IPR001041; Ferredoxin.
DR Pfam: PF00111; fer2; 1.
DR Pfam: PF00037; fer4; 1.
DR TIGRFAMs: TIGR00384; dhsB; 1.
DR PROSITE: PS00198; 4Fe4S_FERREDOXIN; 1.
KW 4Fe-4S; Iron; Iron-sulfur.
SQ SEQUENCE 240 AA; 27529 MW; 02164700BA94C55A CRC64;

Query Match 37.4%; Score 46; DB 1; Length 240;
Best Local Similarity 57.9%; Pred. No. 30;
Matches 11; Conservative 2; Mismatches 4; Indels 2; Gaps 2;

QY 2 GTASCHF-GPLTWCKPQG 19
||| ||| ||| |||
Db 198 GTSRCHFAGECTEVC-PKG 215

RESULT 23

```
Q9HJG6
ID Q9HJG6 PRELIMINARY; PRT; 240 AA.
AC Q9HJG6;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Probable fumarate reductase, subunit B.
GN TA1002.
OS Thermoplasma acidophilum.
OC Archaea; Euryarchaeota; Thermoplasmatata; Thermoplasmatales;
OC Thermoplasmataceae; Thermoplasma.
OX NCBI_TaxID=2303;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 1728;
RX MEDLINE=20479972; PubMed=11029001;
RA Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C.,
RA Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.;
RT "The genome sequence of the thermoacidophilic scavenger Thermoplasma
RT acidophilum."
RL Nature 407:508-513(2000).
DR EMBL; AL445066; CAC12131.1; -.
DR HSSP; PQ0364; 1KF6.
DR InterPro; IPR001450; 4Fe4S_ferredoxin.
DR InterPro; IPR004489; DhsB.
DR InterPro; IPR001041; Ferredoxin.
DR Pfam; PF01111; fer2; 1.
DR Pfam; PF00037; fer4; 1.
DR TIGRFAMs; TIGR00384; dhsB; 1.
DR PROSITE; PS00198; 4FE4S_FERREDOXIN; 1.
KW Iron-sulfur; Complete proteome.
SQ SEQUENCE 240 AA; 27519 MW; AFC645D16995178B CRC64;

Query Match 37.4%; Score 46; DB 17; Length 240;
Best Local Similarity 57.9%; Pred. No. 30;
Matches 11; Conservative 2; Mismatches 4; Indels 2; Gaps 2;

QY 2 GTASCHF-GPLTWCKPQG 19
||: ||| | ||| ||: ||
Db 198 GTSRCHPAGECTEVC-PKG 215

RESULT 24
G33722 PRELIMINARY; PRT; 270 AA.
AC G33722;
DT 01-JAN-1998 (TReMBLrel. 05, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Delta-9 desaturase.
GN DESC.
OS Spirulina platensis.
OC Bacteria; Cyanobacteria; Oscillatoriales; Spirulina.
OX NCBI_TaxID=1156;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C1;
RA Meesapyodsuk D., Deshniun P., Tanticharoen M., Cheevadhanarak S.;
RT "A genetic study of fatty acid desaturation in cyanobacterium
RT Spirulina platensis C1: Temperature regulation of desaturase gene
RT expression."
RL Submitted (OCT-1997) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AJ002065; CAA05166.1; -.
DR InterPro; IPR001522; Desaturase.
DR InterPro; IPR005804; FA_desat_fam.
DR Pfam; PF00487; FA_desaturase; 1.
DR PRINTS; PR00075; FACDDSATRASE.
DR ProDom; PD002221; Desaturase; 1.
SQ SEQUENCE 270 AA; 31406 MW; F4A1DD1576B6F64 CRC64;

Query Match 37.4%; Score 46; DB 2; Length 270;
Best Local Similarity 53.8%; Pred. No. 33;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 2 GTASCHFGPLTWV 14
||: | ||: ||
Db 82 GTLACQGGPIQWV 94

RESULT 25
Q44502 PRELIMINARY; PRT; 272 AA.
ID Q44502;
AC Q44502;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Delta-9 desaturase (Fatty-acid desaturase).
GN DESC OR ALL1599.
OS Anabaena sp. (strain PCC 7120), and
OS Anabaena variabilis.
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690, 1172;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=Anabaena sp. (strain PCC 7120);
RX MEDLINE=21595285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimpō S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium Anabaena sp. strain PCC 7120."
RL DNA Res. 8:205-213(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=A. variabilis;
RX MEDLINE=95014360; PubMed=7929259;
RA Sakamoto T., Wada H., Nishida I., Ohmori M., Murata N.;
RT "Delta 9 Acyl-lipid desaturases of cyanobacteria. Molecular cloning
RT and substrate specificities in terms of fatty acids, sn-positions, and
RT polar head groups."
RL J. Biol. Chem. 269:25576-25580(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=A. variabilis;
RX MEDLINE=94207189; PubMed=8155883;
RA Sakamoto T., Wada H., Nishida I., Ohmori M., Murata N.;
RT "Identification of conserved domains in the delta 12 desaturases of
RT cyanobacteria."
RL Plant Mol. Biol. 24:643-650(1994).
DR EMBL; AP003586; BAB77965.1; -.
DR EMBL; D14581; BAA03434.1; -.
DR InterPro; IPR001522; Desaturase.
DR InterPro; IPR005804; FA_desat_fam.
DR Pfam; PF00487; FA_desaturase; 1.
DR PRINTS; PR00075; FACDDSATRASE.
DR ProDom; PD002221; Desaturase; 1.
KW Complete proteome.
SQ SEQUENCE 272 AA; 31418 MW; E2FBD0CB490D0696 CRC64;

Query Match 37.4%; Score 46; DB 16; Length 272;
Best Local Similarity 53.8%; Pred. No. 33;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 GTASCHFGPLTWV 14
||: | ||: ||
Db 82 GTLACQGGPIQWV 94

RESULT 26
O45177 PRELIMINARY; PRT; 347 AA.
ID O45177;
AC O45177;
DT 01-JUN-1998 (TReMBLrel. 06, Created)
DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)
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DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 40.4 kDa protein.
GN K07H8.8.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
R7 investigating biology. The C. elegans Sequencing Consortium.";
R2 Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Fulton B., Hawkins J., Gattung S., Wohlmann P., Elliott G.;
RT "The sequence of C. elegans cosmid K07H8.";
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RT "Direct Submission.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF047659; AAC04429.1; -.
DR WormPep; K07H8.8; CE18028.
KW Hypothetical protein.
SQ SEQUENCE 347 AA; 40403 MW; AB834716F7FA9963 CRC64;

Query Match 37.4%; Score 46; DB 5; Length 347;
Best Local Similarity 58.3%; Pred. No. 43;
Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 ASCHFGPLTWVC 15
DB 240 ADTHFAPQTWYC 251

RESULT 27
Q8GU51
ID Q8GU51 PRELIMINARY; PRT; 1627 AA.
AC Q8GU51;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE MRP-like ABC transporter (Fragment).
GN MRP11.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Jasinski M., Ducos E., Martinoia E., Boutry M.;
RT "The ATP-binding cassette transporters: structure, function and gene
RT family comparison between rice and Arabidopsis.";
RL Plant Physiol. 0:0-0(0).
DR EMBL; AJ535215; CAD59448.1; -.
FT NON TER 1627
SQ SEQUENCE 1627 AA; 183015 MW; 41635F57BD29AE0E CRC64;

Query Match 37.4%; Score 46; DB 10; Length 1627;
Best Local Similarity 53.8%; Pred. No. 2e+02;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 8 FGPLTWCKPQGG 20
DB 3 FQPLEWYCQVNG 15
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RESULT 28
Q9LTI2
ID Q9LTI2 PRELIMINARY; PRT; 256 AA.
AC Q9LTI2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Gb|AAF01580.1.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Columbia;
RX MEDLINE=20181125; PubMed=10718197;
RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence
RT features of the regions of 3,076,755 bp covered by sixty P1 and TAC
RT clones.";
RL DNA Res. 7:31-63(2000).
DR EMBL; AB025633; BAA97250.1; -.
SQ SEQUENCE 256 AA; 28518 MW; 613226425F06EEB3 CRC64;

Query Match 37.0%; Score 45.5; DB 10; Length 256;
Best Local Similarity 47.4%; Pred. No. 38;
Matches 9; Conservative 2; Mismatches 5; Indels 3; Gaps 1;

QY 2 GTASCHFGPLTWCKPQGG 20
DB 71 GTTSCNF---EWVCHLEDG 86

RESULT 29
Q8XZ32
ID Q8XZ32 PRELIMINARY; PRT; 289 AA.
AC Q8XZ32;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative hydrolase protein (EC 3.-.-.-).
GN RSC1574 OR RS05784.
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Ralstoniaceae; Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GM11000;
RX MEDLINE=21681879; PubMed=11823852;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Arlat M., Billault A., Bröttier P., Camus J.-C., Cattolico L.,
RA Chandler M., Choise N., Claudel-Renard C., Cunnac S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
RA Siguer P., Thebault P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502(2002).
DR EMBL; AL646065; CAD15276.1; -.
DR InterPro; IPR000073; A/b hydrolase.
DR InterPro; IPR003089; AB hydrolase.
DR InterPro; IPR000379; Ser esters_site.
DR Pfam; PF00561; abhydrolase_1.
DR PRINTS; PR00111; ABHYDROLASE.
KW Hydrolase; Complete proteome.
SQ SEQUENCE 289 AA; 31955 MW; F1A7255A3BA146BA CRC64;

Query Match 37.0%; Score 45.5; DB 16; Length 289;
Best Local Similarity 44.4%; Pred. No. 42;
Matches 12; Conservative 1; Mismatches 5; Indels 9; Gaps 2;
```

QY 3 TASCHFGPLT---W-----VCKPQGG 20
 |||||
 :
 167 TISASFGPHTPEQWRALNTAILKPOGG 193

Db

RESULT 30

Q8XZ33 PRELIMINARY; PRT; 323 AA.

AC Q8XZ33;

DT 01-MAR-2002 (TrEMBLrel. 20, Created)

DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Hypothetical protein RSC1573.

GN RSC1573 OR RS05260.

OS Ralstonia solanacearum (Pseudomonas solanacearum).

OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;

OC Ralstoniaceae; Ralstonia.

OX NCBI_TaxID=305;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=GM11000;

RX MEDLINE=21681879; PubMed=11823852;

RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
 Arlat M., Billault A., Brotier P., Camus J.C., Cattolico L.,
 Chandelier M., Choisme N., Claudel-Renard C., Cunnac S., Demange N.,
 Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
 Siguier P., Thebault P., Whalen M., Wincker P., Levy M.,
 Weissenbach J., Boucher C.A.;

RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";

RL Nature 415:497-502(2002).

DR EMBL: AL646065; CAD15275.1; -.

DR InterPro: IPR000073; A/b_hydrolase.

DR InterPro: IPR000379; Ser_estrs_site.

DR Pfam: PF00561; abhydrolase, 1.

KW Hypothetical protein; Complete proteome.

SQ SEQUENCE 323 AA; 35715 MW; C99134AB1216E068 CRC64;

Query Match 37.0%; Score 45.5; DB 16; Length 323;
 Best Local Similarity 44.4%; Pred. No. 47;
 Matches 12; Conservative 1; Mismatches 5; Indels 9; Gaps 2;

QY 3 TASCHFGPLT---W-----VCKPQGG 20
 |||||
 :
 20: TISASFGPHTPEQWRALNTAILKPOGG 227

Db

RESULT 31

Q9LT13 PRELIMINARY; PRT; 356 AA.

AC Q9LT13;

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)

DE Gb|AA01580.1.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.

OX NCBI_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Columbia;

RX MEDLINE=20181125; PubMed=10718197;

RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
 Tabata S.;

RT "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence
 features of the regions of 3,076,755 bp covered by sixty P1 and TAC
 clones.";

RL DNA Res. 7:31-63(2000).

DR EMBL: AB025633; BAA97251.1; -.

SQ SEQUENCE 356 AA; 39393 MW; B4ACB3A06E4C7EC0 CRC64;

Query Match 37.0%; Score 45.5; DB 10; Length 356;
 Best Local Similarity 47.4%; Pred. No. 52;
 Matches 9; Conservative 2; Mismatches 5; Indels 3; Gaps 1;

QY 2 GTASCHFGPLTWVCKPQGG 20
 |||||
 :
 107 GTTSCNF---EWVCHLEDG 122

Db

RESULT 32

O95965 PRELIMINARY; PRT; 494 AA.

AC O95965;

DT 01-MAY-1999 (TrEMBLrel. 10, Created)

DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Ten integrin EGF-like repeat domains protein precursor (ITGBL1).

GN ITGBL1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Fetal lung, and Umbilical vein;

RX MEDLINE=99162403; PubMed=10051402;

RA Berg R.W., Leung E., Gough S., Morris C., Yao W.P., Wang S.X., Ni J.,
 Krissansen G.W.;

RT "Cloning and characterization of a novel beta integrin-related cDNA
 coding for the protein TIED ('ten beta integrin EGF-like repeat
 domains') that maps to chromosome band 13q33: A divergent stand-alone
 integrin stalk structure.";

RT Genomics 56:169-178(1999).

RL [2]

RN SEQUENCE FROM N.A.

RP MEDLINE=22269935; PubMed=12364586;

RX Chumakov I., Blumenfeld M., Guerassimenko O., Cavarec L., Palicio M.,
 Abderrahim H., Bougueleret L., Barry C., Tanaka H., La Rosa P.,
 Puech A., Tahri N., Cohen-Akenine A., Delabrosse S., Lissarrague S.,
 Picard F.-P., Maurice K., Essioux L., Millasseau P., Grel P.,
 Debailleul V., Simon A.-M., Caterina D., Dufaire I., Malekzadeh K.,
 Belova M., Luan J.-J., Bouillot M., Sambucy J.-L., Primas G.,
 Saumier M., Boubkiri N., Martin-Saumier S., Nasroune M., Peixoto H.,
 Delaye A., Pinchot V., Bastucci M., Guillou S., Chevillon M.,
 Sainz-Fuertes R., Meguenni S., Aurich-Costa J., Cherif D., Gimalac A.,
 Van Duijn C., Gauvreau D., Ouellette G., Fortier I., Realson J.,
 Sherbatich T., Riazansky N., Rogaev E., Raeymaekers P., Aerssens J.,
 Konings F., Luyten W., Macchiardi F., Sham P.C., Straub R.E.,
 Weinberger D.R., Cohen N., Cohen D.;

RT "Genetic and physiological data implicating the new human gene G72 and
 the gene for D-amino acid oxidase in schizophrenia.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:13675-13680(2002).

CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).

CC -!- PTM: THE CYSTEINE RESIDUES ARE INVOLVED IN INTRACHAIN DISULFIDE
 BONDS (BY SIMILARITY).

CC -!- SIMILARITY: BELONGS TO THE INTEGRIN BETA CHAIN FAMILY.

DR EMBL: AF072752; AAD17666.1; -.

DR EMBL: AE014302; AAN16024.1; -.

DR HSSP: P05106; 1JV2.

DR InterPro: IPR006209; EGF like.

DR InterPro: IPR001169; Integrin_beta_C.

DR InterPro: IPR002049; Laminin_EGF.

DR PRINTS: PR00011; EGFLAMININ.

DR PROSITE: PS00022; EGF_1; 5.

DR PROSITE: PS01186; EGF_2; 5.

DR PROSITE: PS00243; INTEGRIN_BETA; 10.

KW Cell adhesion; Glycoprotein; Integrin; Repeat; Signal; Transmembrane.

FT SIGNAL 1 23 POTENTIAL.

FT CHAIN 24 494 TEN INTEGRIN EGF-LIKE REPEAT DOMAINS
 PROTEIN.

FT SEQUENCE 494 AA; 53921 MW; 72E095D0BD4ECFF3 CRC64;

Query Match 37.0%; Score 45.5; DB 4; Length 494;


```
DR EMBL; AP003591; BAB74715.1; -.
DR InterPro; IPR001601; Methyltransf.
DR InterPro; IPR000051; SAM_bind.
DR InterPro; IPR004033; Ubie/COQ5_Metrf.
DR Pfam; PF01209; Ubie_methyltran; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 220 AA; 24857 MW; 056081B25C43EB90 CRC64;

Query Match 36.6%; Score 45; DB 16; Length 220;
Best Local Similarity 61.5%; Pred. No. 39;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 8 FGPLTWVCKPQGG 20
   : |||||
Db 131 FAEIKRVCKPQGG 143

RESULT 37
Q8K4K8 PRELIMINARY; PRT; 254 AA.
AC Q8K4K8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Antioxidant protein.
GN PRDX3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvJ;
RA Martinez P., Lescuyer P., Rabilloud T., Lunardi J.;
RT "Characterization of the nuclear gene encoding for the mitochondrial
  antioxidant protein (AOP) from Mus musculus.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
CR EMBL; AF333976; AAM74564.1; -.
DR InterPro; IPR000866; AhpC-TSA.
DR Pfam; PF00578; AhpC-TSA; 1.
SQ SEQUENCE 254 AA; 27686 MW; 7CAF1E6592270B99 CRC64;

Query Match 36.6%; Score 45; DB 11; Length 254;
Best Local Similarity 50.0%; Pred. No. 45;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 7 HFGPLTWVCKPQGG 20
   : |||||
Db 138 HFSLAWINTPNGG 151

RESULT 38
Q07873 PRELIMINARY; PRT; 277 AA.
AC Q07873;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Delta-9 desaturase.
GN DESC.
OS Synecococcus sp. (strain PCC 7002) (Agmenellum quadruplicatum).
OC Bacteria; Cyanobacteria; Chroococcales; Synecococcus.
OX NCBI_TaxID=32049;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97260123; PubMed=9106218;
RA Sakamoto T., Bryant D.A.;
RT "Temperature-regulated mRNA accumulation and stabilization for fatty
  acid desaturase genes in the cyanobacterium Synecococcus sp. strain
  PCC 7002.";
RL Mol. Microbiol. 23:1281-1292(1997).
DR EMBL; U36390; AAB61353.1; -.
DR InterPro; IPR001522; Desaturase.
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DR InterPro; IPR005804; FA_desat_fam.
DR Pfam; PF00487; FA_desaturase; 1.
DR PRINTS; PR00075; FACDDSATRASE.
DR ProDom; PD002221; Desaturase; 1.
SQ SEQUENCE 277 AA; 32207 MW; C88FCA8CC1919A48 CRC64;

Query Match 36.6%; Score 45; DB 2; Length 277;
Best Local Similarity 46.2%; Pred. No. 49;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 GTASCHFGPLTWV 14
   : |||||
Db 82 GTLACQGGPIDWI 94

RESULT 39
Q8LAH5 PRELIMINARY; PRT; 338 AA.
AC Q8LAH5;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Palmitoyl-protein thioesterase-like.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsiis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N.,
RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
RT "Full-length messenger RNA sequences greatly improve genome
  annotation.";
RL Genome Biol. 0:0-0(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
RA Feldmann K.;
RT "Full-length cDNA from Arabidopsis thaliana.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY087806; AAM65342.1; -.
DR InterPro; IPR002472; Palm_thioest.
DR Pfam; PF02089; Palm_thioest; 1.
DR PRINTS; PR00414; PPTHIESTRASE.
SQ SEQUENCE 338 AA; 37136 MW; 10A23369F5AFCCF32 CRC64;

Query Match 36.6%; Score 45; DB 10; Length 338;
Best Local Similarity 57.1%; Pred. No. 59;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 GTASCHFGPLTWVC 15
   : |||||
Db 130 GTASIPFRGATWIC 143

RESULT 40
Q9RRJ7 PRELIMINARY; PRT; 370 AA.
AC Q9RRJ7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Carboxypeptidase G2.
GN DR2493.
OS Deinococcus radiodurans.
OC Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;
OC Deinococcaceae; Deinococcus.
OX NCBI_TaxID=1299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RJ;
RX MEDLINE=20036896; PubMed=10567266;
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RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RT "Genome sequence of the radiocresistant bacterium Deinococcus
RT radiodurans R1.";
RL Science 286:1571-1577(1999);
CR EMBL; AE002078; AAF12031.1; -.
DR HSSP; P06621; ICG2.
DR TIGR; DR2493; -.
DR InterPro; IPR002933; Peptidase_M2C.
DR Pfam; PF01546; Peptidase_M20; 1.
KW Carboxypeptidase; Complete proteome.
SQ SEQUENCE 370 AA; 38831 MW; F45BE553A6694C6D CRC64;

Query Match 36.6%; Score 45; DB 16; Length 370;
Best Local Similarity 80.0%; Pred. No. 65;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QGTASCHFGP 10
Db 58 GGTSRSHFGP 67

RESULT 41
Q8LJS6 PRELIMINARY; PRT; 373 AA.
AC Q8LJS6;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE MOC1.
GN MOC1.
OS Chlamydomonas reinhardtii.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Chlamydomonadaceae; Chlamydomonas.
OX NCBI_TaxID=3055;
RN [1]
RP SEQUENCE FROM N.A.
RA Schoenfeld C., Kruse O.;
RT "Identification of a mtTf-like protein in Chlamydomonas reinhardtii
RT (Moc1).";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF311421; AAM96690.1; -.
DR InterPro; IPR003690; mTERF.
DR Pfam; PF02536; mTERF; 1.
SQ SEQUENCE 373 AA; 40868 MW; FF4654E8450B5479 CRC64;

Query Match 36.6%; Score 45; DB 10; Length 373;
Best Local Similarity 46.7%; Pred. No. 65;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 5 SCHFGPLTWCKPQG 19
Db 358 AAHTGPRRWACEWQG 372

RESULT 42
Q9LGT2 PRELIMINARY; PRT; 534 AA.
AC Q9LGT2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE P0489A01.9 protein.
GN P0489A01.9.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
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OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
RT clone:P0489A01.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP002484; BAA9518.1; -.
DR Gramene; Q9LGT2; -.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 1.
DR SMART; SM00320; WD40; 1.
DR PROSITE; PS00678; WD_REPEATS_1; 1.
DR PROSITE; PS50082; WD_REPEATS_2; 1.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Repeat; WD repeat.
SQ SEQUENCE 534 AA; 60503 MW; 44AD91E9B0DB20BB CRC64;

Query Match 36.6%; Score 45; DB 10; Length 534;
Best Local Similarity 44.4%; Pred. No. 94;
Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 3 TASCHFGPLTWCKPQG 20
Db 276 TMLCHSGPVTAFDRGG 293

RESULT 43
Q9LIEC PRELIMINARY; PRT; 1225 AA.
AC Q9LIEC;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE RNA-dependent RNA polymerase.
GN POL.
OS Lymantria dispar cypovirus 1.
OC Viruses; dsRNA viruses; Reoviridae; Cypovirus.
OX NCBI_TaxID=165803;
RN [1]
RP SEQUENCE FROM N.A.
RA Rao S., Shapiro M., Lynn D., Hagiwara K., Blackmon B., Fang G.,
RA Garner G.R.;
RT "Identification of dsRNA electrophoretotypes of two cypoviruses from a
RT dual infection in gypsy moth, Lymantria dispar.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF389463; AAK73521.1; -.
DR InterPro; IPR007095; RNA_pol_DS_PS.
DR InterPro; IPR007097; RNA_pol_reo.
DR PROSITE; PS50523; RDRP_REO; 1.
DR PROSITE; PS50521; RDRP_VIRAL; 1.
KW RNA-directed RNA polymerase.
SQ SEQUENCE 1225 AA; 138845 MW; 614964068B1AB37D CRC64;

Query Match 36.6%; Score 45; DB 12; Length 1225;
Best Local Similarity 63.6%; Pred. No. 2.1e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 10 PLTWCKPQG 20
Db 833 PLTWLFMPRG 843

RESULT 44
Q8B976 PRELIMINARY; PRT; 1225 AA.
AC Q8B976;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE RNA-dependent RNA polymerase.
OS Dendrolimus punctatus cypovirus 1.
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CC Viruses; dsRNA viruses; Reoviridae; Cypovirus.
OX NCBI_TaxID=208509;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhao S., Liang C., Hong J., Peng H.;
RT "Dendrolimus punctatus CPV segment 2.";
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY147187; AAN46860.1; -.
KW RNA-directed RNA polymerase.
SQ SEQUENCE 1225 AA; 138921 MW; DD480324FCB2A8ED CRC64;

Query Match 36.6%; Score 45; DB 12; Length 1225;
Best Local Similarity 63.6%; Pred. No. 2.1e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 10 PLTWVCKPQGG 20
   ||||| :|||
DB 833 PLTWLFMPRG 843

RESULT 45
Q8YSJ3 PRELIMINARY; PRT; 1290 AA.
AC Q8YSJ3;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Two-component hybrid sensor and regulator.
GN ALR3092.
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21595285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium Anabaena sp. strain PCC 7120.";
RL DNA Res. 8:205-213(2001).
DR EMBL; AP003591; BAB74791.1; -.
DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR004358; Bact_sens_pr_C.
DR InterPro; IPR003661; His_kinA.
DR InterPro; IPR005467; His_kinase.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000700; PAS-assoc_C.
DR InterPro; IPR000014; PAS_domain.
DR InterPro; IPR001789; Response_reg.
DR Pfam; PF02518; HATPase_c; 1.
DR Pfam; PF00512; HSKA; 1.
DR Pfam; PF00785; PAC; 6.
DR Pfam; PF00989; PAS; 5.
DR PRINTS; PFC0072; response_reg; 1.
DR PRINTS; PR00344; BCTRLSENSOR.
DR ProDom; PD000039; Response_reg; 1.
DR SMART; SM00387; HATPase_c; 1.
DR SMART; SM00388; HSKA; 1.
DR SMART; SM00086; PAC; 6.
DR SMART; SM00091; PAS; 5.
DR SMART; SM00448; REC; 1.
DR TIGRfams; TIGR00229; sensory_box; 6.
DR PROSITE; PS50109; HIS_KIN; 1.
DR PROSITE; PS50113; PAC; 6.
DR PROSITE; PS50112; PAS; 5.
DR PROSITE; PS50110; RESPONSE_REGULATORY; 1.
KW Complete proteome.
SQ SEQUENCE 1290 AA; 144892 MW; FC0BDC7CBDE58E2B2 CRC64;

Query Match 36.6%; Score 45; DB 16; Length 1290;
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CC Viruses; dsRNA viruses; Reoviridae; Cypovirus.
OX NCBI_TaxID=208509;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhao S., Liang C., Hong J., Peng H.;
RT "Dendrolimus punctatus CPV segment 2.";
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY147187; AAN46860.1; -.
KW RNA-directed RNA polymerase.
SQ SEQUENCE 1225 AA; 138921 MW; DD480324FCB2A8ED CRC64;

Query Match 36.6%; Score 45; DB 10; Length 1494;
Best Local Similarity 37.5%; Pred. No. 2.6e+02;
Matches 6; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCK 16
   ||| | :|||
DB 290 GGRGGCYRAVVSWLCK 305

RESULT 47
Q9C8G9 PRELIMINARY; PRT; 1622 AA.
AC Q9C8G9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Glutathione S-conjugate transporting ATPase (AtMRP1).
GN T4K22.12.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC euroids II; Brassicales; Brassicaceae; Arabidopses.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=cv. Columbia;
RX MEDLINE=21016719; PubMed=11130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Lueros J.S., Maiti R., Marziani A.,
RA Miltscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
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Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
 RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.,
 RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
 RT thaliana";
 RL Nature 408:816-820(2000).
 CC -!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
 DR EMBL; AC025295; AAG51096.1; -;
 DR InterPro; IPR003593; AAA_ATPase.
 DR InterPro; IPR001140; ABC_TM_transpt.
 DR InterPro; IPR003439; ABC_TM_transporter.
 DR Pfam; PF00664; ABC_membrane; 2.
 DR Pfam; PF00005; ABC_tran; 2.
 DR ProDom; PD000006; ABC_transporter; 1.
 DR SMART; SM00382; AAA; 2.
 DR PROSITE; PS00211; ABC_TRANSPORTER; 2.
 KW ATP-binding; Transport.
 SQ SEQUENCE 1622 AA; 181925 MW; B71E085798F1BBD6 CRC64;
 Query Match 36.6%; Score 45; DB 10; Length 1622;
 Best Local Similarity 70.0%; Pred. No. 2.8e+02;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 8 FGPLTWVCKP 17
 Db 3 FEPLDWYCKP 12
 RESULT 48
 Q24635 PRELIMINARY; PRT; 1622 AA.
 AC Q24635;
 DT 01-JAN-1998 (TREMBLrel. 05, Created).
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update).
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update).
 DE Multidrug resistance-associated protein homolog.
 GN MRP1.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids 1; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN 1;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97368351; PubMed=9223346;
 RA Lu Y.P., Li Z.S., Rea P.A.;
 RT "AtMRP1 gene of Arabidopsis encodes a putative ABC-conjugate pump;
 RT isolation and functional definition of a plant ABC binding cassette
 RT transporter gene.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:8243-8248(1997).
 RN 2;
 RP SEQUENCE FROM N.A.
 RA Lu Y.P., Li Z.-S., Rea P.A.;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 RN 3;
 RP SEQUENCE FROM N.A.
 RA Lu Y.-P., Li Z.-S., Rea P.A.;
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
 DR EMBL; AF038125; AAB71832.1; -;
 DR EMBL; AF08124; AAB67319.1; -;
 DR InterPro; IPR003593; AAA_ATPase.
 DR InterPro; IPR001140; ABC_TM_transpt.
 DR InterPro; IPR003439; ABC_TM_transporter.
 DR Pfam; PF00664; ABC_membrane; 2.
 DR Pfam; PF00005; ABC_tran; 2.
 DR ProDom; PD000006; ABC_transporter; 1.
 DR SMART; SM00382; AAA; 2.
 DR PROSITE; PS00211; ABC_TRANSPORTER; 2.
 KW ATP-binding; Hydrolase; Transport.
 SQ SEQUENCE 1622 AA; 182015 MW; 6F0287AF651AD5CF CRC64;
 Query Match 36.6%; Score 45; DB 10; Length 1622;
 Best Local Similarity 70.0%; Pred. No. 2.8e+02;

Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 8 FGPLTWVCKP 17
 Db 3 FEPLDWYCKP 12
 RESULT 49
 Q26008 PRELIMINARY; PRT; 2910 AA.
 AC Q26008;
 DT 01-NOV-1996 (TREMBLrel. 01, Created).
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update).
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update).
 DE RNA polymerase I.
 OS Plasmodium falciparum.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5833;
 RN 1;
 RP SEQUENCE FROM N.A.
 RC STRAIN=Honduras I;
 RX MEDLINE=94081864; PubMed=8259131;
 RA Fox B.A., Li W.B., Tanaka M., Inselburg J., Bzik D.J.;
 RT "Molecular characterization of the largest subunit of plasmodium
 RT falciparum RNA polymerase I.";
 RL Mol. Biochem. Parasitol. 61:37-48(1993).
 DR EMBL; L11172; AAA72349.1; -;
 DR InterPro; IPR006592; RNA_polA_N.
 DR InterPro; IPR000722; RNA_pol_A.
 DR InterPro; IPR007080; RNA_pol_Rpb1_1.
 DR InterPro; IPR007066; RNA_pol_Rpb1_3.
 DR InterPro; IPR007083; RNA_pol_Rpb1_4.
 DR InterPro; IPR007081; RNA_pol_Rpb1_5.
 DR Pfam; PF04997; RNA_pol_Rpb1_1; 1.
 DR Pfam; PF00623; RNA_pol_Rpb1_2; 1.
 DR Pfam; PF04983; RNA_pol_Rpb1_3; 1.
 DR Pfam; PF05000; RNA_pol_Rpb1_4; 1.
 DR Pfam; PF04998; RNA_pol_Rpb1_5; 1.
 DR SMART; SM00663; RPOA_N; 1.
 SQ SEQUENCE 2910 AA; 340170 MW; AF838248497DAB22 CRC64;
 Query Match 36.6%; Score 45; DB 5; Length 2910;
 Best Local Similarity 60.0%; Pred. No. 5e+02;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 7 HFGPLTWVCK 16
 Db 2702 HFSPVTWLK 2711
 RESULT 50
 Q8I410 PRELIMINARY; PRT; 2914 AA.
 ID Q8I410
 AC Q8I410;
 DT 01-MAR-2003 (TREMBLrel. 23, Created).
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update).
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update).
 DE RNA polymerase I.
 GN PFE0465C.
 OS Plasmodium falciparum (isolate 3D7).
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=36329;
 RN 1;
 RP SEQUENCE FROM N.A.
 RA Devlin K., Baker S., Davies P., Mungal K., Berriman M., Pain A.,
 RA Hall N., Bowman S., Churcher C., Quail M., Barrell B.;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RN 2;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22255708; PubMed=12368867;
 RA Hall N., Pain A., Berriman M., Churcher C., Harris B., Harris D.,
 RA Mungall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K.,
 RA Buckee C.O., Burrows C., Cherevach I., Chillingworth C.,

RA Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C.,
RA Cronin A., Davies R., Davis P., Dear P., Dearden F., Doggett J.,
RA Feltwell T., Goble A., Goodhead I., Gwilliam R., Hamlin N., Hance Z.,
RA Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P.,
RA Humphray S., Jagels K., James K.D., Johnson D., Kerhornou A.,
RA Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,
RA Line A., Maddison M., Mclean J., Mooney P., Moule S., Murphy L.,
RA Oliver K., Ormond D., Price C., Quail M.A., Rabinowitsch E.,
RA Rajandream M.A., Rutter S., Rutherford K.M., Sanders M., Simmonds M.,
RA Seeger K., Sharp S., Smith R., Squares R., Squares S., Stevens K.,
RA Taylor K., Tivey A., Unwin L., Whitehead S., Woodward J.,
RA Suiston J.E., Craig A., Newbold C., Barrelli B.G.;
RT "Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13.";
RL Nature 419:527-531(2002).
DR EMBL: AL929352; CAD51459.1; -.
SQ SEQUENCE 2914 AA, 340672 MW, 7ED0547CCBF376EE CRC64;

Query Match 36.6%; Score 45; DB 5; Length 2914;
Best Local Similarity 60.0%; Pred. No. 5.1e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 7 HFGPLTWCK 16
|||:|:|
Db 2703 HFSPVTWILK 2712

Search completed: November 5, 2003, 19:06:45
Job time : 38 secs